

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 15:10:37 : Search time 5976.93 Seconds

(Without alignments)
5756.003 Million cell updates/sec

Title: US-09-581-241-3

Perfect score: 1644
Sequence: 1 atggaataatgatgagaacga.....agaacacgttgtaagatg 1644

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_bhg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vl:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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RESULT	1	1644	100.0	1644	6	E36479	E36479 Luciferase
LOCUS	E36479	1640.8	99.8	1644	6	E36480	E36480 Luciferase
DEFINITION	E36479	1639.2	99.7	1644	6	AR098258	AR098258 Sequence
ACCESSION	E36479	1636	99.5	1644	6	E02495	E02495 cDNA encodi
VERSION	E36479	1636	99.5	1644	6	E05448	E05448 cDNA sequen
KEYWORDS	E36479	1636	99.5	1644	6	E05448	E05448 cDNA sequen
SOURCE	E36479	1636	99.5	1644	6	E05448	E05448 cDNA sequen
ORGANISM	E36479	1636	99.5	1644	6	E05448	E05448 cDNA sequen
REFERENCE	E36479	1636	99.5	1644	6	E05448	E05448 cDNA sequen
AUTHORS	E36479	1636	99.5	1644	6	E05448	E05448 cDNA sequen
TITLE	E36479	1636	99.5	1644	6	E05448	E05448 cDNA sequen
JOURNAL	E36479	1636	99.5	1644	6	E05448	E05448 cDNA sequen
COMMENT	E36479	1636	99.5	1644	6	E05448	E05448 cDNA sequen
OS	E36479	1636	99.5	1644	6	E05448	E05448 cDNA sequen
PN	E36479	1636	99.5	1644	6	E05448	E05448 cDNA sequen
PD	E36479	1636	99.5	1644	6	E05448	E05448 cDNA sequen
PF	E36479	1636	99.5	1644	6	E05448	E05448 cDNA sequen
PR	E36479	1636	99.5	1644	6	E05448	E05448 cDNA sequen

ALIGNMENTS

RESULT 1
LOCUS E36479
DEFINITION Luciferase and method for assaying intracellular ATP by using the

Same.

ACCESSION E36479
VERSION E36479.1 GI:13022686
KEYWORDS JP 1999239493-A/3.

SOURCE JP 1999239493-A/3.
ORGANISM Luciferia lateralis.

Luciferia lateralis
Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
Pterygota: Neoptera: Endopterygota: Coleoptera: Polyphaga:
Elateriformia: Cantharoidae: Lampyridae: Luciferia.

1 (bases 1 to 1644)
Noriaki,H.S.M.M.
Luciferase and method for assaying intracellular ATP by using the

Patent: JP 1999239493-A 3 07-SEP-1999;

KIKKOMAN CORP

OS Luciferia lateralis

PN JP 1999239493-A/3

PD 07-SEP-1999

PF 21-DEC-1998 JP 1998363108

PR

PI NORIARI HATTORI, SEIJI MURAKAMI
 PC C12N15/09, C12N9/02, C1201/66//C12N9/02, C12N1:19), C12N15/00 CC
 FH Key Location/Qualifiers
 CDS (1): .(1644).
 FEATURES
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 /organism="Luciola lateralis"
 /db_xref="taxon:7052"
 BASE COUNT 528 a 261 c 349 g 506 t
 ORIGIN

Query Match 100.0%; Score 1644; DB 6; Length 1644;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggaacaatggaagaacatgaataatggtatggtcctgaacatttaccctatt 60
 DB 1 atggaacaatggaagaacatgaataatggtatggtcctgaacatttaccctatt 60
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 DB 61 gaagaagagatgctgtagacacattgccaagatataatgatgatgaataaacttga 120
 QY 121 gcaattgtcttacttaacgacttaccggtgtcgtatatacgtacgccaataactaga 180
 DB 121 gcaattgtcttacttaacgacttaccggtgtcgtatatacgtacgccaataactaga 180
 QY 181 aatcagctgctgtaggaagaagccttaagaataatggtgtgtgtgtgtgtgtgtgt 240
 DB 181 aatcagctgctgtaggaagaagccttaagaataatggtgtgtgtgtgtgtgtgtgt 240
 QY 241 gscattatgcaatgaagaacatgtaagaattcttattccctgattagccggttattata 300
 DB 241 gscattatgcaatgaagaacatgtaagaattcttattccctgattagccggttattata 300
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 DB 301 ggtgtcgt 360
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 DB 361 ggcattctcgaagccaacatttatttatttataaagaagattgataaagtataact 420
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 DB 421 gtaacaaaaacggtactgctataaaccattgttataatgagcgaagatggtat 480
 QY 481 agaggttataatcactgaagacacttataaagaacactccacaaggtttcaagga 540
 DB 481 agaggttataatcactgaagacacttataaagaacactccacaaggtttcaagga 540
 QY 541 tcaagttttaaacctgtaagaatgtaacgccaagaagaaggtgctcttaataatgact 600
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 DB 721 actgtagtaccatccatcactgattgtgtatgttactacttggtgctatctactgt 780
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 DB 901 gaattactcataaataatgattatcaaatgtgtgaattgcaatctggtcggaaccc 960
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 DB 961 ttatctaaagaatltgtgaagcgtgtgtcagaacgtttaaattaccgggtgtgtc 1020
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 DB 1021 ggtcattgtttaaacaagaacacccctgcaattattataccaccggaagcgatgataa 1080
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 QY 1141 aaaaaaaccttggccccaagaagcgtgtgaaggtgtgtgaaggtcctatgtatg 1200
 DB 1141 aaaaaaaccttggccccaagaagcgtgtgaaggtgtgtgaaggtcctatgtatg 1200
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 DB 1201 aaggttattatgaataatccagaagcaacaagaagaataatcagatgaagaaggtgtgtg 1260
 QY 1261 caacagaagatattgtgtattacgaatgaagaagaacatttcttactcgtgtgactgt 1320
 DB 1261 caacagaagatattgtgtattacgaatgaagaagaacatttcttactcgtgtgactgt 1320
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 DB 1321 aagctttaaataaataaagaagataatgaatccaccctgctgaattgaattcgttct 1380
 QY 1381 ttgcaacatccaaataatlttctgacgagcgtgtgctgaggtccatccatcactgactgt 1440
 DB 1381 ttgcaacatccaaataatlttctgacgagcgtgtgctgaggtccatccatcactgactgt 1440
 QY 1441 gagctccgggagcgt 1500
 DB 1441 gagctccgggagcgt 1500
 QY 1501 atggaattcgttctgactgaagtttcaaatgcaaaacgttttcgtgtgtgtgtgtgtgt 1560
 DB 1501 atggaattcgttctgactgaagtttcaaatgcaaaacgttttcgtgtgtgtgtgtgtgt 1560
 QY 1561 gtgagcgaagtaacttaaggtctcaactgtgttaaatgtacgtgaagaacatlaagaata 1620
 DB 1561 gtgagcgaagtaacttaaggtctcaactgtgttaaatgtacgtgaagaacatlaagaata 1620
 QY 1621 ctgaagaacacagttgtcgaagt 1644
 DB 1621 ctgaagaacacagttgtcgaagt 1644

RESULT 2
 E36480 1644 bp DNA linear PAT 07-FEB-2001
 LOCUS E36480
 DEFINITION Luciferase and method for assaying intracellular ATP by using the same.
 ACCESSION E36480
 VERSION E36480.1 GI:13022687
 KEYWORDS JP 1999239493-A/4.
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia; Cantharidoidea; Lampyridae; Luciola.
 REFERENCE 1 (bases 1 to 1644)
 Noriaki, H.S.M.M.
 TITLE Luciferase and method for assaying intracellular ATP by using the

Unclassified.
1 (bases 1 to 1644)
Hirokawa, K., Kajiyama, N. and Murakami, S.
TITLE
Mutant-type bioluminescent protein, and process for producing the
JOURNAL
Patent: US 6074859-A 13 13-JUN-2000;
FEATURES
Location/Qualifiers
1..1644

BASE COUNT 528 a 260 c 350 g 506 t
ORIGIN

Query Match 99.7%; Score 1639.2; DB 6; Length 1644;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1641; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 atggagaaacatggagagacatgaataatgtgtatgtccggaaccatttaccctatt 60
DB 1 ATGGAGAAACATGGAGACATGAAATATGTGTATGTGCTGTAACCATTTTACCTATT 60
QY 61 gaagaaggatctgtgagacacattgcgaagtatatgatcgatatgcaaaacttga 120
DB 61 GAAGAGAGATCTGTGAGACACATTGCCAANTATATGATGATATGCAAACTTGA 120
QY 121 gcaatgtcttactaaacgacttaccggtgtcgaattacgtaacgacgaactagaa 180
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DB 181 AATCATGCTGTCTAGAGAGCGCTTTAAAGAAATTATGTGTTGTTGTTGAAGAAATT 240
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DB 841 GATTACAAATGTTCAACCGGTATTCTTGTACCCACTTTGTTGCATTTCTTAATAGAGAT 900
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DB 1081 CCAAGTGCTCTTGCAGAAAGTTGTGCCATTATTTAAAGCAAAAGCTTATCGATCTGTACT 1140
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DB 1141 AAAAAAATTTGGCCCGGACAGACACTGAGAAAGTTGTGTAAGGCTCTTATGCTTATG 1200
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DB 1261 CACACAGGAGATTTGTTGATTAGATGAAGAAACAAATTTCTTTATCGATCGCTTTG 1320
QY 1321 aagttcttaacaaatacaagaagataccaagtcacacgtcgtatataatgttctt 1380
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DB 1381 TTGCAACATCCAAATTTTCTGTACGCCGCTGTGCGGTTCCAAATCCTATAGCTGTG 1440
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QY 1501 atggattacgttgcgtgaagtttcaaatgtcaaacggtttgcgtgtgtgtgtgtgt 1560
DB 1501 ATGGATTACGTTGCTGCTGCTCAAGTTTCAAAATGCAAAACGTTTGGTGCTGTGCTGCTTT 1560
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DB 1621 CTGAAGAACACAGTTGTCTAAGATG 1644

RESULT 4
LOCUS E02495 1644 bp RNA linear PAT 29-SEP-1997
DEFINITION cDNA encoding luciferase.
ACCESSION E02495
VERSION E02495.1 GI:2170725
KEYWORDS JP 1990171189-A/1.
SOURCE
ORGANISM
Luciola lateralis.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Elateriformia; Cantharoidea; Lampyridae; Luciola.
REFERENCE
AUTHORS
Kajiyama, N., Tatsumi, H. and Nakano, E.
TITLE
LUCIFERASE GENE
JOURNAL
Patent: JP 1990171189-A 1 02-JUL-1990;

COMMENT KIKKOMAN CORP
 OS Luciola lateralis
 PN JP 1990171189-A/1
 PD 02-JUL-1990
 PF 22-DEC-1988 JP 1988322029
 PI KAIJIYAMA NAOKI, TATSUMI HIROKI, NAKANO EIICHI PC
 CI2N5/33//CI2N9/02:
 CC strandedness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 FH Key
 FT mat-peptide 1..1644
 FT /product='Luciferase',
 FT Location/Qualifiers
 source 1..1644
 /organism='Luciola lateralis'
 /db_xref='taxon:7052'
 BASE COUNT 529 a 262 c 349 g 504 t
 ORIGIN

Query Match 99.5%; Score 1636; DB 6; Length 1644;
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 Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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 Db 361 GGCATCTCAAGCAACATTGATTTGTCTTAAAAAGATTAGATTAAGTTTAACT 420
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 Db 421 GTACAAAAACGGTACGTCTATLAAAACATTGTATATTGAGACGAAGTGGATTAT 480
 QY 481 agaggtatcaatcactgacacatttataaaaaaacactcacaaggtttcaaga 540
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 Db 601 TCGGTTCAACGGTTTGCAAAAGTGCTGAACCTACTACTAGAATAATTGCTACTAGA 660
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 Db 901 GAATTACTCGATAAATGATTATATCAAAATTAGTTGAATTTGCATCTGGCGAGACCT 960
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 Db 1141 AAAAAAACCCTTGGCCCGCAACAGCGTGCAGAGTGTGTGTAAGGCTCTATGCTTTAG 1200
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 QY 1261 cacacagagagatgtgtgttactcgaatgaagaacacatttcttactgtgtgtgtgt 1320
 Db 1261 CACACAGAGAGATGTGTGTACTCGAATGAAGAACACATTCTTTACGTGATCGTTGT 1320
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 QY 1381 ttgcaacatccaatattttttagtgcgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1440
 Db 1381 TTGCAACATCCAAATATTTTGAATGCCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
 QY 1441 gagcttcgagagctgt 1500
 Db 1441 GAGCTTCGAGAGCTGT 1500
 QY 1501 atggaatcgttctgaatcaagtttcaaaagcaaaagtttgggtgtgtgtgtgtgtgt 1560
 Db 1501 ATGGAATCCTTCTGAATCAAGTTTCAAAAGCAAAAGTTTGGCTGTGTGTGTGTGTGTGT 1560
 QY 1561 gtgagcaagatgacttaaggtctcactgtgtgaattgaacgttaagaacattagaata 1620
 Db 1561 GTGAGCAAGATGACTTAAAGGTCTCCTACTGTGTGAATTGACGTTAAAGCAATTAGAGAATA 1620
 QY 1621 ctgaagaacacagttgtctaaagt 1644
 Db 1621 CTGAAGAACAACAGTTGTCTAAGATG 1644

RESULT 5
 E05448 E05448 1644 bp RNA linear PAT 29-SEP-1997
 LOCUS
 DEFINITION CDNA sequence of luciferase.
 ACCESSION E05448
 VERSION E05448.1 GI:2173637

Db	481	ACAGGTTATCAATCCATGAGCAAACTTTATTAATAAAAAACATCCACAGGTTTCAAAAGA	540
OY	541	tcaagttttaaaccgttgaagttaaacccgaagaacaaagttgcttataatgaactc	600
Db	541	TCAAAGTTTAAACGTGTGAAGATTACCGCAAAACAAAGTTGCTCTTATTAATGAACCTC	600
OY	601	tccgggtlcaaacccggtttgccaagaagtggtgaacttactcaatgaanaattggtcactaga	660
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Db	661	TTTTTCTCACGCTAGAGATCCAAATTATGGAACCAAGTTTCCACGAGCAAGGCTATTATTA	720
OY	721	actgtagatcacattccatcalcgtgtttgtgtatgttactaacttlaagctactcaactgt	780
Db	721	ACTGTAGTACCAATCCATCAATGCTTTGGTGTCTTTACTCTTTAGGCTATCTAACCTGG	780
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OY	841	gattacaaatgtlcaaaagcgttatctctgtlacccgcacttgtgtcgaatttctaaatagaat	900
Db	841	GATTACAATGTTCAAGGCTATCTCTTGACCGACTTGTTCGAANTCTTATPATAAGT	900
OY	901	gaattaccgcgtlaaatatgattatcaaatlttagtgaatgtcatctgcygagcacct	960
Db	901	GAATTACTCGATTAATATGATTTATCAAAATTTAGTTGAAATTCATCTGCGGACACCT	960
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OY	1021	ggtctatggttttaacagaacaacactctgcaattatlatcacccggaagcgatgataa	1080
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OY	1141	aaaaaacttgggcccgaacagacgltggaagaagtttgltgaagaagtlcctatgcttatg	1200
Db	1141	AAAAAACTTTGGGCCCCGACAGACGCGGAGAGTTTGTGTAAGAGGTCCTATGCTTATG	1200
OY	1201	aaaagttatgtagaatactcagaagcaacaagaagaatcatagatgaaagaagttggtg	1260
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OY	1441	gaagttccgggaagctgtgtgttgaacttaagaaaggaanaatcatgaactgaaagaagta	1500
Db	1441	GAGGTTTCCGGGAACTGTGTGTTGACTTTGAAAAAGGAAAAATCTATGACTGAAAAAAGTA	1500
OY	1501	atgagttacgcttgctatgcgaagtttccaatatgcanaacgcttgcgtgtgtgtccgttt	1560
Db	1501	ATGAGTTACGCTTCTGTGTAAGTTTCAATGCAAAACGTTTGCGTGTGTGTCCGTTT	1560
OY	1561	gttggaacgaagttacctaaagcttccactgtttaaattgacgltaaagcaattagagaata	1620
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Qy 1621 ctgaagaacacagttgtcgaatg 1644

Db 1621 CTGAAGAAACAGTGTGCTTAAGATG 1644

RESULT 6

LOCUS LLLUCI 1781 bp mRNA linear INV 24-NOV-1993

DEFINITION L. lateralis luciferase mRNA.

ACCESSION X66919.38389

VERSION X66919.1 GI:9526

KEYWORDS luciferase.

SOURCE Japanese firefly.

ORGANISM Eucloia lateralis

REFERENCE 1 (bases 1 to 1781)
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia; Cantharoidea; Lampyridae; Luciola.

REFERENCE 2 (bases 1 to 1781)
Tatsumi, H., Kaijima, N. and Nakano, E.
Molecular cloning and expression in Escherichia coli of a cDNA clone encoding luciferase of a firefly, Luciola lateralis Biochim. Biophys. Acta 1131 (2), 161-165 (1992)

REFERENCE 3
Tatsumi, H.
Direct Submission
Submitted (21-JUL-1992) H. Tatsumi, Research and Development Division, Kikkoman Corporation, 399 Noda, Noda City, Chiba 278, JAPAN

FEATURES

source location/Qualifiers

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59..1705 /product="luciferase"

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BASE COUNT 579 a 276 c 367 g 559 t

ORIGIN

Query Match 99.5%; Score 1636; DB 3; Length 1781;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 239 AATCATGCTGCTAGAGAGGCTTTAAAGAAATATGTTGGTTGATGGAAGAAAT 298

Qy 241 ggcgttcagtgaaacacgttgaaatcttattccgttattagccggttattata 300

Db 299 GCGTTATGACAGTAAACCTGTGAAGATCTTATTCTCTGATTTAGCCGTTATTATA 358

Qy 301 ggtcgttgatgctcacaatagatattacactcactcagtgaaattggttcacagtta 360

Db 359 GGTGTGCGTGTGCTCAACTATGAGATTATGACCTCTAGCAATTTGGTTCACAGTTTA 418

Qy 361 ggcactcctaaccaacaattgattagttcctaaaaaggtatgataaagtataact 420

Db 419 GGCATCTCTAAGCCAACTATGATTAGTTCTTAAAAAGGATTAATTAAGTTATTAAC 478

Qy 421 gtcaaaaaacggttaactgctattaaacattgattatttgacagcaagtgtat 480

Db 479 GTCAAAAAACGGTAACCTGCTATTAAACCATTTGTTATGACAGCAAGGATTTAT 538

Qy 481 agaggtatcatcatcagacacttattataaaaaacacatccacaaggttcaaaaga 540

Db 539 AGAGCTTATCAATCCATGACACACTTTATAAAAAACCTCCACAGGTTCAAGA 598

Qy 541 tcaaggtttaaactctagaagttaacccgaagaagaagttgcttataatgaact 600

Db 599 TCAAGTTTAAACTGTAGAAATTAAACCCGAAGAACAACTCTTATTAATGAACCT 658

Qy 601 tcggttcacacggttgctgcacaaaggttgcaacttaccatgaataatttgctactga 660

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Qy 661 ttcttcacgctagaatcccaatttataagaacaagtttcacagcaaggttattta 720

Db 719 TTTTCTCAGCGTGAAGATTCATTTATGGAACCAAGTTTACACAGCAGCGCTATTATA 778

Qy 721 actgtatgacatccatcactatggttggatgattactactttaggtctactaactgt 780

Db 779 ACTGTATGACATTCATCATATGATGTTGTGATGTTTACTTATAGCTATCACTTGT 838

Qy 781 ggttctgctatgcatgcttgaacgaataattgacgaagaagctttttaaacaacgtgca 840

Db 839 GGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 898

Qy 841 gattacaatgcttgaacgcttattctgttgaacgacttgttgcaattcttataagaat 900

Db 899 GATTACAAGTGTAAACGCTTATCTGTGACCGCTTGTGGAATTTTAAATAGAGT 958

Qy 901 gaattactcgaataatgattatcactaaattgattgaaattgacatcgtggaagcact 960

Db 959 GAATTACTCGATTAATATGATTTATCAAAATTTAGTTAAATTCATCTGCGGAGACCT 1018

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Db 1019 TTATCTAAGAAATTTGTAAGCTGTTGCTTAGACGTTTATTTACCGGGTGTTCGCA 1078

Qy 1021 gctatgctttaaacaacaacactcgtcaattatcaacacccgaagcgatgataa 1080

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RESULT 8
AR062709
LOCUS AR062709 1908 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 8 from patent US 5843746.
ACCESSION AR062709
VERSION AR062709.1 GI:5990400
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1908)
AUTHORS Tatsumi, H., Fukuda, S., Kikuchi, M. and Koyama, Y.
TITLE Biotinlated firefly luciferase, a gene for biotinated firefly luciferase, a recombinant DNA, a process for producing biotinated luciferase and a bioluminescent analysis method
JOURNAL Patent: US 5843746-A 8 01-DEC-1998;
FEATURES
Location/Qualifiers
1..1908
source /organism="unknown"
BASE COUNT 598 a 329 c 426 g 555 t
ORIGIN

Query Match 99.2%; Score 1631.4; DB 6; Length 1908;
Best Local Similarity 99.6%; Pred. No. 0;
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Db	1501	ATGGATTACGTTGTCAGTCAAGTTCAAATGCAAAACGTTTCGTGTGTGTCCGCTTTT	1560
QY	1561	gtggacgaagtagtcctaaagctgtcactggttaaatgtgacgtgtaagcaattagagaata	1620
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LOCUS	El2279	1908 bp	DNA linear PAT 24-JUN-1998
DEFINITION	CDNA encoding biotinylated Luciola luciferase.		
ACCESSION	El2279		
VERSION	El2279.1 GI:3251113		
KEYWORDS	JP 1996308578-A/4.		
SOURCE	Luciola lateralis.		
ORGANISM	Luciola lateralis		
REFERENCE	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia; Cantharoidae; Lampyridae; Luciola.		
AUTHORS	1 (bases 1 to 1908)		
TITLE	Tatsumi,H., Fukuda,M., Kikuchi,M. and Koyama,T.,		
JOURNAL	BIOTIN FIRE FLY LUCIFERASE, BIOTIN FIRE FLY LUCIFERASE GENE, NEW RECOMBINANT DNA, PRODUCTION OF BIOTIN FIRE FLY LUCIFERASE AND BIOLUMINESCENCE ANALYSIS		
COMMENT	Patent: JP 1996308578-A 4 26-NOV-1996; KIKKOMAN CORP		
OS	Luciola lateralis		
PN	JP 1996308578-A/4		
PD	26-NOV-1996		
PF	24-APR-1995 JP 1995098857		
PR	27-JUL-1994 JP 94P 193798, 14-MAR-1995 JP 95P 54625		
PT	TANSUMI H,ROTH F, FUKUDA MASARU, KIKUCHI MANORU, KOYAMA TAJUT PC		
CI	121M15/09,C12M9/02,C12Q1/26,(C12M9/02,C12R1:185); CC		
CC	strandedness: Double;		
CC	Topology: Unknown;		
CC	hypoetical: No;		
CC	anti-sense: No;		
FM	Key	Location/Qualifiers	
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ORIGIN	598 a 329 c 426 g 555 t		
Query Match	99.2%; Score 1631.4; DB 6; Length 1908;		
Best Local Similarity	99.6%; Pred. No. 0;		
Matches 1635; Conservative	0; Mismatches 6; Indels 0; Gaps 0;		
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Qy	1141	aaaaaaactltgggcccgaacacagctgtagaag	tttctgtlaaaggtlccctatgtctatg	1200
Dd	1141	AAAAAAACTTTGGGCGCGGAACAGCGTGGAGAA	GGTTGTGTAAGGCTCTATGCTTATG	1200
Qy	1201	aaaggtatgtatgataatccagaagaacaaga	gaaalcatagatgaagaagttgtgtg	1260
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 Db 1321 AAGCTTTAAATCAATATCAAAAGGATATATAGTACCACTGCTGATTTGAATCTCTTT 1380
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 Db 1561 GTGAGCAGAGTACTAAAGGCTCTCACTGTAATTTGACGGTAAGCAATTAGAGAAATA 1620
 QY 1621 ctgaagaacacagctgtcgaag 1641
 Db 1621 CTGAAGAAACAGCTGTCTAG 1641

RESULT 10

LOCUS E16288 1920 bp DNA linear PAT 28-JUL-1999
 DEFINITION DNA encoding fusion protein which comprises luciferase and
 lysostaphin.

ACCESSION E16288.1 GI:5710971
 VERSION JP 1998150991-A/1.
 KEYWORDS unclassified.
 SOURCE unclassified.
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1920)
 AUTHORS Tatsumi,H., Fukuda,M. and Nagahara,A.
 TITLE LUCIFERASE-LYOSTAPHRIN FUSED PROTEIN, ITS PRODUCTION AND
 BIOIMMUNESCENT ANALYSIS USING THE SAME
 JOURNAL Patent: JP 1998150991-A 1 09-JUN-1998;
 KIKKOMAN CORP

COMMENT

OS None
 OC Artificial sequences.
 PN JP 1998150991-A/1
 PD 09-JUN-1998
 PF 25-NOV-1996 JP 1996328042
 PI TATSUMI HIROKI, FUKUDA MASARU, NAGAHARA AYUMI PC
 C12N15/09,C07H21/04,C07K19/00,C12N9/02,C12N9/52,C12P21/02, PC
 C1201/66,
 PC (C12N9/02,C12R1:19),(C12N9/52,C12R1:19);
 CC strandedness: Double;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No; Location/Qualifiers

FT source 1..1920
 FT 1..1920 /organism='Artificial sequences'.
 FEATURES source Location/Qualifiers

BASE COUNT 627 a 310 c 407 g 576 t
 ORIGIN /organism="unidentified"
 /db_xref="taxon:32644"

Query Match

99.2%; Score 1631.4; DB 6; Length 1920;

Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1635; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 atggaacacatggagacagatgaataatgtgtatgttccttaacattaccatt 60
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 Db 61 GAAGAGAGATCGTCTGAGACACATTGCCAAGTATATGATGATGCAAAACCTTGGA 120
 QY 121 gcaattccttactaaagcactaccggtgtcgtatatacgtacgcgaataactgaag 180
 Db 121 GCAATTCTGTTTACTTAACGACACTACCGGTGTGATATACGACGCAATGACTTAAGAA 180
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 QY 241 gcgtatgcagtgaaacactgaaagaaatccttataccttataagccggtttatata 300
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 QY 301 ggtgctcgt 360
 Db 301 GGTGCTCGGT 360
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 Db 361 GGCATTCTTAAGCCACACATTTGTATTTAGTTTAAAGAGATTAGTATGATTATTAAT 420
 QY 421 gtacaaaaacggtacactgctataaaacattgttatatgagacgaagaatgagat 480
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CC	PF	27-APR-1994 JP 1994090275	
CC	PI	TATSUMI HIROKI, FUKUDA MASARU	
CC	PC	C12N15/09, C07K14/36, C07K19/00, C12P21/02, G01N33/53, (C12P21/02,	
CC	CC	C12R1:19);	
CC	CC	Strandedness: Double;	
CC	CC	topology: Linear;	
CC	CC	hypothetical: No;	
CC	CC	anti-sense: No;	
CC	CC	Key	Location/Qualifiers
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CC	CC	FT	Best Local Similarity 98.7%; Score 1623.2; DB 23; Length 2019;
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OY	9	catgagaagaatgaataatctgctatgctgctgctgaacacattacaccttaagaagg	68
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OY	69	atctgctgagacaaattgcgaagatatagatalcgaatgcataaacttgagacaaattgc	128
Db	444	ATCTGCTGAGACACAATGTCGCCAAGTATATGAGATCGATATGCAAAACCTTGACCAATGTC	503
OY	129	tttaactaagcacttaccggtgcgcatttaagtaagtaagcgcgaacttagaaaaatcatg	188
Db	504	TTTTACTAGCACACTTACCGGTGCGATTATACCTAGCGCGAATCTTAAATAATCATG	563
OY	189	ctgctcagagagagccttaagaatctatggtctgctgctgagagaattgcgtatg	248
Db	564	CTGCTAGGAGAGAGCGCTTAAAGATTATATGTTGTTGTTGATGGAAGATTGCGTTAG	623
OY	249	cagtgaaacagctgaagaattcttactctgatttagccggtttattatagtgctgg	308
Db	624	CAGTGAATACTGTGAAGGTTCTTATCTGTTATTAAGCCGGTTTATTTATTAAGTGTGCG	683
OY	309	tctgtctcacaactatagatcttaccactcagctgaaattggttcacagtttagacatc	368
Db	684	TGTGCTGCCAATCATATGAGATTAACTACCTAGCGAATTGTTCCACAGTTTAGCATCTC	743
OY	369	taagccaacaattgattatctgctcctaagaagaattagataaagtataactaglacaaa	428
Db	744	TAAAGCCACAATGTTATTTGTTCTTAAAAAAGGATTAGATAAAGTTATTAACGTACAAAA	803
OY	429	aacggttaacgctatataaacacattgatatatggacagcaagaatgagattagaggtta	488
Db	804	AAGGTTAAGCGTATTTAAACCATTTGTTATTTGGACAGCAAGTGCATTATAGAGGTTA	863
OY	489	tcaatcagtagacaacttataaaaaaaacactccacaaggttccaagaatccaagttt	548
Db	864	TCAATTCATGAGACAACCTTTATTTAAAAAAAACATCCACAAGGTTTCAAGGATCAAGTTT	923
OY	549	taaacagtagaagtttaacccgaagaagaacagttgctcttataatgaactcttggttc	608
Db	924	TAAAACTGTGAAGTTTAAACCGCAAAAGACAAGTGTCTTTATTAATGAACCTTCTCGGTTCC	983
OY	609	aaccggtttgccaaaagggtgtgcaacttaactaataagaatttggtaacagattttctca	668
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QY 789 tatgtcatgttaacgaaatttgacgaagagactttttaaaaaaacctgcgaagatacaa 848
DB 1164 TATTGTCAATGTTAAAGAAATTTGACGAAGAGACTTTTAAACACATGCAAGATTACAA 1223
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QY 1509 cgttgcacgtcaagtttcaaatgcaaaacgttttcgtgtgtgtgtcgttttgggagga 1568
DB 1884 CGTGTGCTAGTCAAGTTTCAATGCAAAACGTTTCCGTGTGTGTGCTTGTGGAGAGA 1943
QY 1569 agtaacctaaaggtctcaactgttaaatgacgtgaaagcaattagagaatctagaaga 1628
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QY 1629 accagttgctaagatg 1644
DB 2004 ACCAGTTGCTAAGATG 2019

RESULT 12
E10170 ID E10170 standard: DNA; UNC: 2055 BP.

XX AC E10170:
XX SV E10170.1
XX DT 08-OCT-1997 (Rel. 52, Created)
XX DT 02-SEP-2000 (Rel. 65, Last updated, Version 2)
XX DE DNA encoding mutated streptavidin-firefly luciferase fusion protein.
XX KW JP 1995289264-A/2.
XX OS unidentified
XX OC unclassified.
XX RN [1]
XX RP 1-2055
XX RA Tatsumi H., Fukuda M.;
XX RT "VARIANT TYPE STREPTAVIDIN GENE, FUSION PROTEIN GENE OF VARIANT TYPE
XX STREPTAVIDIN-FIREFLY LUCIFERASE, NEW RECOMBINANT AND PRODUCTION OF FUSION
XX PROTEIN OF VARIANT TYPE STREPTAVIDIN-FIREFLY LUCIFERASE";
XX RL Patent number JP1995289264-A/2, 07-NOV-1995.
XX RL KIKKOMAN CORP.
XX OS None
XX CC Artificial sequences.
XX CC PN JP 1995289264-A/2
XX CC PD 07-NOV-1995
XX CC PF 27-APR-1994 JP 1994090275
XX CC PI TATSUMI HIROKI, FUKUDA MASARU
XX CC PC C12N15/09, C07K14/36, C07K19/00, C12P21/02, G01N33/53, C12P21/02,
XX CC C12R1:19;
XX CC CC strandedness: Double;
XX CC topology: Linear;
XX CC hypothetical: No;
XX CC anti-sense: No;
XX CC key Location/Qualifiers
XX FH source 1..2055
XX FT /organism="Artificial sequences"
XX CC CDS
XX CC FT 1..2055
XX CC FT /product="mutated streptavidin-firefly
XX CC FT luciferase fusion
XX CC FT protein"
XX FH Key Location/Qualifiers
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Query Match 98.7%; Score 1623.2; DB 23; Length 2055;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1628; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 9 catgagaacgatgaanaatatgtatgtatgtctgaacatttaaccattatgaagagg 68
DB 420 CCTCGAAGCATGAAATFATGTATGTATGTCCTGAACCATTTTACCCATTTGAAGAGG 479
QY 69 atctgtgtgagacaattgtgcgaagatlatatgatcatatgcaaaacttgagagaattgc 128
DB 480 ATCTGCTGAGACACAATTGCCCAAGTATATGATGATGATGCAAAACTTGGAGCAATTGC 539
QY 129 tttaactaacgacttacgggtgtctgattatagatgacgcgaataactagaanaatcatg 188
DB 540 TTTTACTAACGCACTTACCGGTGTGATATATACGATTAACCGCAATATCTTGAAGAAATCATG 599
QY 189 ctgtctagagagagctttaagaatlatatgtgtgtgtgtgtgtatgagaaatgtcgtatg 248
DB 600 CTGTCTAGAGAGGCTTTAAAGAAATTTATGTTGGTGTGTATGAGAAATTCCTATAG 659

QY 249 cagtgaaacgtgaaagattcttcttctgattagccggtttatattagtggtcg 308
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 Db 660 CAGTGAAACCTGTGAAGAGTCTTTATTCCTGTATTAAGCCGGTTATTTATATAGTGTGCG 719
 QY 309 tctgtgctcaactaatgaaattctacactacgtgaattggttcacagtttaagcctc 368
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 Db 720 TCTGTGCTCAACTAATGAAATTTACACTCTAGTGAAATTTGGTTCAAGTTTAGCATCTC 779
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 Db 780 TAAGCCAAACAAATTTATTTAGTTCTTAAAAAGATTAGATTAAGTTATTAACGTACAAA 839
 QY 429 aacggttaactgctattaaacacattgttattgagcaagcaagttgattatagaatt 488
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 Db 900 TCAATCCATGSAACACTTTATTAAAAAACACTCCACAAGTTTCAAGGATCAAGTTT 959
 QY 549 taaactgtagaagtttaaccgcaagaagaagttgctcttataatgaactctcggttc 608
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RESULT 13
 AR043316
 LOCUS AR043316 1704 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 5 from patent US 5814465.
 ACCESSION AR043316
 VERSION AR043316.1 GI:5964324
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1704)
 AUTHORS Tatsumi, H., Fukuda, S., Kikuchi, M. and Koyama, Y.
 TITLE Biotinlated firefly luciferase, a gene for biotinlated firefly luciferase, a recombinant DNA, a process for producing biotinlated luciferase and a bioluminescent analysis method
 JOURNAL Patent: US 5814465-A 5 29-SEP-1998.
 FEATURES
 source Location/Qualifiers
 BASE COUNT 541 a 275 c 361 g 527 t
 ORIGIN
 Query Match 98.7%; Score 1622.8; DB 6; Length 1704;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1627; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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 Db 131 CTGCTGAGACCAATTGCCAGATATATGATGATGATGATGATGATGATGATGATGATGAT 190
 QY 131 ttactaacgacttaccggtgtcgtattatatacgaacgcaatctttagaanaatctgtc 190
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 Db 191 TTACTTAACGCACTTACCGGTGCTGATTTATGATGATGATGATGATGATGATGATGATGAT 250
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 QY 251 gtgaacactgtgaagaattcttattctcgttattagcgggttattatagagtgctggt 310
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 Db 311 GTGAAGACGTGAAGAGTCTTTATTCCTGATTAAGCGGCTTATTATTATGATGATGATGAT 370
 QY 311 tggctccaactaatgagatttacaactctacgtgaattgtgttcaagttttagcatctcta 370

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Db 371 TGGCTCCAACTAATGAGATTATACCTACGTGAATTGGTCCACAGTTTGGCGATCTCTA 430
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Db 431 AGCCACAACTATTGTTATTTAGTTCTTAAAAAGSATTAGATTAAGTTATATACGTACAAAAA 490
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Oy 1271 atatgggtatcatagatgaagaagaaacatctcttactgtgagacgtttgaagtttaa 1330
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RESULT 14
AR062708
LOCUS AR062708 1704 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5843746.
ACCESSION AR062708
VERSION AR062708.1 GI:5990399
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1704)
AUTHORS Tatsumi,H., Fukuda,S., Kikuchi,M. and Koyama,Y.
TITLE Biotinized firefly luciferase, a gene for biotinated firefly luciferase, a recombinant DNA, a process for producing biotinated luciferase and a bioluminescent analysis method
Patent: US 5843746-A 5 01-DEC-1996;
JOURNAL Location/Qualifiers
FEATURES
source 1..1704
BASP COUNT 541 a 275 c 361 g 527 t
ORIGIN

Query Match 98.7%; Score 1622.8; DB 6; Length 1704;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1627; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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 LOCUS E12278
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 ACCESSION E12278
 VERSION E12278.1 GI:3251112
 KEYWORDS JP 1996308578-A/3.
 SOURCE Luciola lateralis.
 ORGANISM Luciola lateralis.
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 Elateriformia; Cantharoidea; Lampyridae; Luciola.
 REFERENCE
 AUTHORS Tatsumi,H., Fukuda,M., Kikuchi,M. and Koyama,T. .
 TITLE 1 (bases 1 to 1704)
 BIOTIN FIRE FLY LUCIFERASE, BIOTIN FIRE FLY LUCIFERASE GENE, NEW
 RECOMBINANT DNA, PRODUCTION OF BIOTIN FIRE FLY LUCIFERASE AND
 BIOLUMINESCENCE ANALYSIS
 Patent: JP 1996308578-A 3 26-NOV-1996;
 KIKROMAN CORP
 JOURNAL
 COMMENT
 OS Luciola lateralis
 PN JP 1996308578-A/3
 PD 26-NOV-1996
 PF 24-APR-1995 JP 1995098857
 PR 27-JUL-1994 JP 94P 193798, 14-MAR-1995 JP 95P 54625 PT
 TATSUMI HIROKI, FUKUDA MASARU, KIKUCHI MAMORU, KOYAMA TAJIJI PC
 C12N15/09,C12N9/02,C12Q1/26,(C12N9/02,C12R1.185); CC
 strandedness: Double;
 CC topology: Unknown;
 CC hypothetical: No;
 CC anti-sense: No;
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 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1627; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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 Db 1631 TACCTAAAGGCTCTCAGTGGTAAATTTGACGTTAAACCAATTAGAGAAATACTGAGAAAC 1690
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 Db 1691 CAGTTGCTAAGATG 1704

Search completed: September 6, 2002, 19:27:48
 Job time: 15431 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 16:39:12 : Search time 512.01 Seconds
(without alignments)
5512.797 Million cell updates/sec

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Perfect score: 1644
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1636	99.5	1644	14	AAQ34745
5	1632.8	99.3	1644	14	AAQ34745
6	1631.4	99.2	1908	18	AAQ3257
7	1631.4	99.2	1920	19	AAV32467
8	1623.2	98.7	2019	17	AAV3850
9	1623.2	98.7	2055	17	AAV3851

10	1622.8	98.7	1704	18	AAV63268
11	1622.8	98.7	1704	19	AAV23595
12	1621.6	98.6	2364	19	AAV23580
13	1493.6	90.9	1556	20	AAV25717
14	1356	82.5	1644	10	AAV91170
15	1356	82.5	1644	11	AAQ03801
16	1356	82.5	1644	12	AAQ13844
17	1356	82.5	1644	22	AAQ92231
18	1356	82.5	1644	24	AAQ22186
19	1354.4	82.4	1644	14	AAQ13825
20	1354.4	82.4	1644	12	AAQ34987
21	1352.8	82.3	1644	12	AAQ13840
22	1352.8	82.3	1644	12	AAQ13841
23	1352.8	82.3	1644	12	AAQ13842
24	1352.8	82.3	1644	12	AAQ13843
25	1352.8	82.3	1644	12	AAQ13845
26	1263.2	76.8	1656	20	AAV25716
27	1040.8	63.3	1656	20	AAV25715
28	1016	61.8	1970	16	AAV00613
29	748.4	45.5	10533	16	AAQ98930
30	748.4	45.5	10558	16	AAQ98912
31	748	45.5	6565	22	AAV55126
32	748	45.5	6971	22	AAV55124
33	748	45.5	7558	22	AAV55125
34	748	45.5	7969	22	AAV55123
35	745.8	45.4	5427	22	AAV83390
36	745.2	45.3	1811	15	AAQ58732
37	745.2	45.3	5620	18	AAV48630
38	745.2	45.3	5620	22	AAV30233
39	745.2	45.3	5789	20	AAV08779
40	745.2	45.3	5791	20	AAV08778
41	745.2	45.3	5793	20	AAV08776
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43	745.2	45.3	5818	21	AAV38352
44	745.2	45.3	5819	20	AAV08775
45	745.2	45.3	5819	20	AAV08774

ALIGNMENTS

RESULT	ID	AAx84395 standard; DNA; 1644 BP.	ALIGNMENTS
XX	AAx84395		
XX	AAx84395:		
AC	09-SEP-1999 (first entry)		
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XX	L. lateralis luciferase coding sequence.		
DE	Luciferase; surfactant-tolerant; firefly; intracellular ATP assay; ss.		
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OS	Luciola lateralis.		
XX			
PN	WO9933997-AI.		
XX			
PD	08-JUL-1999.		
XX			
PF	24-DEC-1998; 98WO-JP05864.		
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PR	26-DEC-1997; 97JP-0361022.		
XX			
PA	(KIKK) KIKKOMAN CORP.		
XX			
PI	Hattori N, Murakami S;		
XX			
DR	WPI; 1999-419109/35.		
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DR	P-PsDB; AAV22182.		
XX			
PT	Modified luciferase tolerant to surfactants and useful for assay of		
XX	intracellular ATP		

Firefly luciferase
Antibody-Firefly 1
Antibody-Firefly 1
Firefly luciferase
Recombinant luciferase
Luciferase mutant
Modified luciferase
Luciola cruciata 1
Luciferase. Lucio
Thermotable lucif
Luciferase mutant
Luciferase mutant
Luciferase mutant
Luciferase mutant
Luciferase mutant
Firefly luciferase
Firefly luciferase
DNA encoding lucif
Vector p39neoluc s
TGF-beta responsiv
Nucleotide sequenc
Nucleotide sequenc
Nucleotide sequenc
Nucleotide sequenc
Luciferase reporte
Encodes firefly lu
Ad5-ITR, CMV-lucif
Minimal adenovirus
pGL2-Promoter gene
pGL2(GST-ARE)SV40/
pGL2(apo AI-ARE)SV
pGL2(apo AI-mare)S
Plasmid pGL2 (apoa
pGL2(apo AI-491 mu
pGL2(apo AI-250)lu

PS Example 2; Page 34-39; 56pp; English.
XX This sequence encodes a *Luciola lateralis* luciferase of the invention.
CC The protein is a surfactant-tolerant luciferase which is derived from
CC firefly luciferase by replacement of the glutamic acid residue at
CC position 490 by another amino acid. The luciferase can be used in an
CC assay of intracellular ATP in biological samples containing cells, for
CC example for establishing the presence of cells, and their quantity, in
CC the sample. The method can be applied to foodstuffs, drugs,
CC agrochemicals, beverages and environmental samples. The activity of the
CC surfactant-tolerant luciferase is not lowered by the presence of high
CC concentrations of surfactant and therefore an assay of high accuracy can
CC be carried out in a simple manner.
XX

Sequence 1644 BP; 528 A; 261 C; 349 G; 506 T; 0 other;

Query Match 100.0%; Score 1644; DB 20; Length 1644;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 atggaacacatgagagacatgaaatattgtatgctgcctgaaccatttaccctatt 60
DB 1 atggaacacatgagagacatgaaatattgtatgctgcctgaaccatttaccctatt 60
QY 61 gaagaggaatctgctggaacacatgacgaatgatatgatgcgatacgaaacttga 120
DB 61 gaagaggaatctgctggaacacatgacgaatgatatgatgcgatacgaaacttga 120
QY 121 gcaattgctttacttaacgcgaacttcacggtgtcogattacgtaacggaacttagaa 180
DB 121 gcaattgctttacttaacgcgaacttcacggtgtcogattacgtaacggaacttagaa 180
QY 181 aatcatgctgctcctgaagagagctttaagaattatgctgttggtttatggaagaatt 240
DB 181 aatcatgctgctcctgaagagagctttaagaattatgctgttggtttatggaagaatt 240
QY 241 gcgttatgcagtgaacaaactgtgaagaattccttattcctgtatagccggttatttata 300
DB 241 gcgttatgcagtgaacaaactgtgaagaattccttattcctgtatagccggttatttata 300
QY 301 ggtgtcgggtgtgtcccaactatgagatttacactctacgtaagtgttgcacattta 360
DB 301 ggtgtcgggtgtgtcccaactatgagatttacactctacgtaagtgttgcacattta 360
QY 361 ggcattctcaagccaacaaactgtattatgctcttaaaaaagagattagataaagtataact 420
DB 361 ggcattctcaagccaacaaactgtattatgctcttaaaaaagagattagataaagtataact 420
QY 421 gtacaaaaaaacggttaactgtatlaaaacacattgtatataatgacagcaaatgagattat 480
DB 421 gtacaaaaaaacggttaactgtatlaaaacacattgtatataatgacagcaaatgagattat 480
QY 481 agagttttcaatcatalgacacactttatlaaaaaaaacccccaagaagtttcaaga 540
DB 481 agagttttcaatcatalgacacactttatlaaaaaaaacccccaagaagtttcaaga 540
QY 541 tcaagttttaaaactgtlaagaatttaacccaagaacaagttgctcttataatgaactct 600
DB 541 tcaagttttaaaactgtlaagaatttaacccaagaacaagttgctcttataatgaactct 600
QY 601 tcgggttcaaacgggtttcccaaaaaggtgtgcaacttactcatgaaatttgcactaga 660
DB 601 tcgggttcaaacgggtttcccaaaaaggtgtgcaacttactcatgaaatttgcactaga 660
QY 661 tttttcagctagagatccaattatgaaacaaagtttccacggcagcgtatttta 720
DB 661 tttttcagctagagatccaattatgaaacaaagtttccacggcagcgtatttta 720
QY 721 actgtatgacacatccatcatatggtttgtgtaagttaactacttaggcataacttgt 780
DB 721 actgtatgacacatccatcatatggtttgtgtaagttaactacttaggcataacttgt 780
```

```
QY 781 gtttcgtatgtcatgttaacgaatattgacgaagaagacttttaaaacacgtgcaa 840
DB 781 gtttcgtatgtcatgttaacgaatattgacgaagaagacttttaaaacacacgtgcaa 840
QY 841 gattacaatgttcaacggttattcttctgtacgcgaacttgttgcgaattcctaagaagt 900
DB 841 gattacaatgttcaacggttattcttctgtacgcgaacttgttgcgaattcctaagaagt 900
QY 901 gaattctcgaataaataatgattatacaaatattgattgaattgaattcactgacggcgaacct 960
DB 901 gaattctcgaataaataatgattatacaaatattgattgaattgaattcactgacggcgaacct 960
QY 961 ttactcaagaagaatttgtgaagctgtgtgtagacggttttaattaccgggtgtgtcga 1020
DB 961 ttactcaagaagaatttgtgaagctgtgtgtagacggttttaattaccgggtgtgtcga 1020
QY 1021 ggtcatgttttaacagaagaacacactctgcaattatatacaccggaagcgatgataa 1080
DB 1021 ggtcatgttttaacagaagaacacactctgcaattatatacaccggaagcgatgataa 1080
QY 1081 ccagggtgcttctgtgcaagaagtgtgccaattatttaagaacaaagttacgacttgatct 1140
DB 1081 ccagggtgcttctgtgcaagaagtgtgccaattatttaagaacaaagttacgacttgatct 1140
QY 1141 aaaaaaaccttggcccgacacagacgtggaagaattgtgtlaaaggtccatgctatg 1200
DB 1141 aaaaaaaccttggcccgacacagacgtggaagaattgtgtlaaaggtccatgctatg 1200
QY 1201 aaagttatgtatagataatccagaagaacagaagaatacatagatgaagaagttgttg 1260
DB 1201 aaagttatgtatagataatccagaagaacagaagaatacatagatgaagaagttgttg 1260
QY 1261 cacacagagatatttggatattacagatgaagaagaacatttcttactgtgagctgttg 1320
DB 1261 cacacagagatatttggatattacagatgaagaagaacatttcttactgtgagctgttg 1320
QY 1321 aagttcttaatacaataacagaagatatacaagtaaccacctgtgtaattagaatctgtctt 1380
DB 1321 aagttcttaatacaataacagaagatatacaagtaaccacctgtgtaattagaatctgtctt 1380
QY 1381 ttgcaacatcccaaatatttttgaatgcggcggtgtgcgggttcccaatccataagctgtg 1440
DB 1381 ttgcaacatcccaaatatttttgaatgcggcggtgtgcgggttcccaatccataagctgtg 1440
QY 1441 gagcttcgggagcgtgtttgttgaacttaagaagaagaatctatgactgtaaaagaagta 1500
DB 1441 gagcttcgggagcgtgtttgttgaacttaagaagaagaatctatgactgtaaaagaagta 1500
QY 1501 atggaattacgttgtcagtaagttcaaatgcaaaaacgtttgcgtgtgtgcgtttt 1560
DB 1501 atggaattacgttgtcagtaagttcaaatgcaaaaacgtttgcgtgtgtgcgtttt 1560
QY 1561 gtggaagaagtaacctaaagttctcaatgtaaatattgaacggttaagaacattagaagaata 1620
DB 1561 gtggaagaagtaacctaaagttctcaatgtaaatattgaacggttaagaacattagaagaata 1620
QY 1621 ctgaagaaacccagttgctaagatg 1644
DB 1621 ctgaagaaacccagttgctaagatg 1644
```

RESULT 2
AAx84396
ID AAx84396 standard; DNA; 1644 BP.
XX
XX AAx84396;
AC
XX
XX 09-SEP-1999 (first entry)
DT
XX
XX L. lateralis luciferase coding sequence.
DE
XX
XX Luciferase; surfactant-tolerant; firefly; intracellular ATP assay; ss.
XX

OS Luciola lateralis.
 XX MO9933997-A1.
 XX 08-JUL-1999.
 PD 24-DEC-1998; 98WO-JP05864.
 XX 26-DEC-1997; 97JP-0361022.
 PR (KIKK) KIKKOMAN CORP.
 XX Hattori N, Murakami S;
 XX WPI: 1999-419109/35.
 DR P-PSDB: AAY22183.
 XX
 PT Modified luciferase tolerant to surfactants and useful for assay of
 PT intracellular ATP
 XX
 PS Example 2; Page 43-48; 56pp; English.
 CC This sequence encodes a Luciola lateralis luciferase of the invention.
 CC The protein is a surfactant-tolerant luciferase which is derived from
 CC firefly luciferase by replacement of the glutamic acid residue at
 CC position 490 by another amino acid. The luciferase can be used in an
 CC assay of intracellular ATP in biological samples containing cells, for
 CC example for establishing the presence of cells, and their quantity, in
 CC the sample. The method can be applied to foodstuffs, drugs,
 CC agrochemicals, beverages and environmental samples. The activity of the
 CC surfactant-tolerant luciferase is not lowered by the presence of high
 CC concentrations of surfactant and therefore an assay of high accuracy can
 CC be carried out in a simple manner.
 XX
 SO Sequence 1644 BP; 529 A; 262 C; 348 G; 505 T; 0 other;

Query Match 99.8%; Score 1640.8; DB 20; Length 1644;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1642; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 atggaacaatggaagacatgaaatattgtatggtcctgaacatttaccatt 60
 Db 1 atggaacaatggaagacatgaaatattgtatggtcctgaacatttaccatt 60
 QY 61 gaagaggatctgctgagcacaattggcgaagtatagtgatgacgacaaacttga 120
 Db 61 gaagaggatctgctgagcacaattggcgaagtatagtgatgacgacaaacttga 120
 QY 121 gcaattgctttactaacgcaactccggtgcgaattacgtacgcgcgaacttagaa 180
 Db 121 gcaattgctttactaacgcaactccggtgcgaattacgtacgcgcgaacttagaa 180
 QY 181 aaatcatgctgtctagagagcgtttaagaattatggttggttgtatgtagaagaatt 240
 Db 181 aaatcatgctgtctagagagcgtttaagaattatggttggttgtatgtagaagaatt 240
 QY 241 ggttatcgaatgaaactgtgaagaattcttattcctgatttagccggtttattata 300
 Db 241 ggttatcgaatgaaactgtgaagaattcttattcctgatttagccggtttattata 300
 QY 301 ggtgcgtgtgctgcacaactaatgattacactcactgaatgattggtcacagttta 360
 Db 301 ggtgcgtgtgctgcacaactaatgattacactcactgaatgattggtcacagttta 360
 QY 361 ggcattcctaagccaactatgtattatgcttcttaaaaaaggaattagataaagtataact 420
 Db 361 ggcattcctaagccaactatgtattatgcttcttaaaaaaggaattagataaagtataact 420
 QY 421 gtacaaaaaagctaacgtacttaaaacattgttatattatgacagaagaagtgtatatt 480
 Db 421 gtacaaaaaagctaacgtacttaaaacattgttatattatgacagaagaagtgtatatt 480

QY 481 agagttatcatccatggaacaatttataaaaaaacctccacaaggtttcaaga 540
 Db 481 agagttatcatccatggaacaatttataaaaaaacctccacaaggtttcaaga 540
 QY 541 tcaagtttaaaacgttagaagtttaacccgaagaacaggtgtcttataatgaact 600
 Db 541 tcaagtttaaaacgttagaagtttaacccgaagaacaggtgtcttataatgaact 600
 QY 601 tcgggttcaacccggtttgcacaaaggtgtgcaacttaccatgaataatttgcactaga 660
 Db 601 tcgggttcaacccggtttgcacaaaggtgtgcaacttaccatgaataatttgcactaga 660
 QY 661 ttcttcacgttagagatccaatltatggaaaacaaagttcacacgacgactattta 720
 Db 661 ttcttcacgttagagatccaatltatggaaaacaaagttcacacgacgactattta 720
 QY 721 actgttagaccattccatcgtgtttgtgtatgttttaccatttaagctatcctaattgt 780
 Db 721 actgttagaccattccatcgtgtttgtgtatgttttaccatttaagctatcctaattgt 780
 QY 781 ggtttcgtatgtcatgttaacgaatttgacgaagacgtttttaaaacactgcac 840
 Db 781 ggtttcgtatgtcatgttaacgaatttgacgaagacgtttttaaaacactgcac 840
 QY 841 gattacaatgttcaacgcttattctgttacccgacttgttgcaattccttaataagaat 900
 Db 841 gattacaatgttcaacgcttattctgttacccgacttgttgcaattccttaataagaat 900
 QY 901 gaattactcagataatattgtttatcaaatattgttgaaattgcatctgacggaagact 960
 Db 901 gaattactcagataatattgtttatcaaatattgttgaaattgcatctgacggaagact 960
 QY 961 ttactcaagaatattgttgaagctgtgttagacgttttaattaccggtgtgtcaca 1020
 Db 961 ttactcaagaatattgttgaagctgtgttagacgttttaattaccggtgtgtcaca 1020
 QY 1021 ggtcattgtttaacagaacaacactctgcataattatcaacacggaagcgatgataa 1080
 Db 1021 ggtcattgtttaacagaacaacactctgcataattatcaacacggaagcgatgataa 1080
 QY 1081 ccaggtgtctctgcaagttgtgccaattttaagaacaaattatcgtctgtgact 1140
 Db 1081 ccaggtgtctctgcaagttgtgccaattttaagaacaaattatcgtctgtgact 1140
 QY 1141 aaaaaaactttggcccggaacagacgtggaagattgtttaaagggtccatgactatg 1200
 Db 1141 aaaaaaactttggcccggaacagacgtggaagattgtttaaagggtccatgactatg 1200
 QY 1201 aaagttatgttagataatccagaagaacaagaataatcatalgagaagggtgtgtg 1260
 Db 1201 aaagttatgttagataatccagaagaacaagaataatcatalgagaagggtgtgtg 1260
 QY 1261 caccacagagatattgtgttattacgtagaagaataattcttattcgtgagctgttg 1320
 Db 1261 caccacagagatattgtgttattacgtagaagaataattcttattcgtgagctgttg 1320
 QY 1321 aagctttaatcaatacaagaatgatcaagttaccacgtctggaattagatattgttctt 1380
 Db 1321 aagctttaatcaatacaagaatgatcaagttaccacgtctggaattagatattgttctt 1380
 QY 1381 ttgcaacatccaaatattttgtatgctgcggtgtgtgtgtccagatccatagctgtgt 1440
 Db 1381 ttgcaacatccaaatattttgtatgctgcggtgtgtgtgtccagatccatagctgtgt 1440
 QY 1441 gagcttccggagctgtgtgtgttattacctaagaagaataatctatgactggaagaagta 1500
 Db 1441 gagcttccggagctgtgtgtgttattacctaagaagaataatctatgactggaagaagta 1500
 QY 1501 atgattacgtgtgttagtcaagttcaaatgcaaaacgtttgtgtgtgtgtgtgtgt 1560
 Db 1501 atgattacgtgtgttagtcaagttcaaatgcaaaacgtttgtgtgtgtgtgtgtgtgt 1560
 QY 1561 gtggacgaagtacttaagaaggttcatcgtgttaaaattgacggtlaaagaatttagaata 1620

Db	1261	caacacgggaatacttgggtaattacgctgaagaaacattcttaccgtggacggtttg	1320
Qy	1321	aagttcttaacaaatacaaaagataccaaagataccacctgtcgtaaattgaatctgttctt	1380
Db	1321	aagttcttaacaaatacaaaagataccaaagataccacctgtcgtaaattgaatctgttctt	1380
Qy	1381	ttgcaacatccaatttttttgatagccggcgctgtgtggttccagatccctatagctggt	1440
Db	1381	ttgcaacatccaatttttttgatagccggcgctgtgtggttccagatccctatagctggt	1440
Qy	1441	gagcttcgggaagctgttctgttgaacctaaaggaagaaactatgaactgaaagaagta	1500
Db	1441	gagcttcgggaagctgttctgttgaacctaaaggaagaaactatgaactgaaagaagta	1500
Qy	1501	atggattacgttctgtctgttcaagtttcaaatgcgaaaagtttgcgtggtggtgtccgtttt	1560
Db	1501	atggattacgttctgtctgttcaagtttcaaatgcgaaaagtttgcgtggtggtgtccgtttt	1560
Qy	1561	gtggagcgaagtacctaaagatccctacctgtgtaaatgtacgcgtgaagacaaatagaagaaata	1620
Db	1561	gtggagcgaagtacctaaagatccctacctgtgtaaatgtacgcgtgaagacaaatagaagaaata	1620
Qy	1621	ctgaagaaccagttgctgaagatg	1644
Db	1621	ctgaagaaccagttgctgaagatg	1644

RESULT 4

AAQ34745

ID AAQ34745 standard; cDNA to mRNA; 1644 BP.

AC AAQ34745;

DT 24-MAY-1993 (first entry)

Thermostable luciferase (wild-type).

Firefly; *Luciola cruciata*; GENJI; *Luciola lateralis*; HEIKE;

KW mutant; assay; ss.

05 *Luciola lateralis*.

PN EP524448-A.

27-JAN-1993.

AA	
PF	26-JUN-1992; 92EP-0110808.

XX 27-JUN-1991: 91JP-0157117

PR	29-NOV-1991;	9LUP-031/064
PR	22-MAY-1992:	92JP-0131057

XX
PA (KTKK) KTKKMAN CORP.

Naoki K.
Fujichi N.
XX
PT

XX WPT: 1993-038553/04
DP

DR P-PSDB; AAR30803.

PT New DNA sequence

PT replaced by a hydrophobic aminoacid

PS Claim 1-3; Page 29-30 + 21-24; 33pp; English.

A DNA sequence of a thermostable luciferase of a firefly, which encodes the amino acid sequence of a wild-type firefly luciferase in which an amino acid at the 217 position or an amino acid at the position equiv. to the 217 position of the luciferase of *Luciola cruciata* (GNNJ firefly) of *Luciola lateralis* (HEIKE firefly) is replaced by a hydrophobic amino acids, esp. Ile, Leu or Val, is claimed. The mutant luciferases identical in properties to the

CC wild-type luciferase except that it is stable when heated to high
CC temps., e.g. 50 degrees C. The luciferase can be used in assays for
CC e.g. ATP.
XX
SQ Sequence 1644 BP; 529 A; 262 C; 349 G; 504 T; 0 other;

Query Match	99.5%;	Score 1636;	DB 14;	Length 1644;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 1639; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

QY	1	atggaacaacatgaggaagacagatagaaataatggtatgattggtctctgaacattttacccatt	60
Db	1	atggaacaacatgaggaagacagatagaaataatggtatgattggtctctgaacattttacccatt	60
QY	61	gaagaggatctcgctcgagagccaattcgcaagatatatgatctgatatagtcaaaccttga	120
Db	61	gaagaggatctcgctcgagagccaattcgcaagatatatgatctgatatagtcaaaccttga	120
QY	121	gcaatttgctttacthaacgcacactaacogtgcgtatatacgtiacgcgcgaatacttaga	180
Db	121	gcaatttgctttacthaacgcacactaacogtgcgtatatacgtiacgcgcgaatacttaga	180
QY	181	aaatcaatcgtctctagaggaagagctttaagaatatggtttggtttgtatgtagaagaatt	240
Db	181	aaatcaatcgtctctagaggaagagctttaagaatatggtttggtttgtatgtagaagaatt	240
QY	241	gcgtatcagatggaanaactcgtggaagaattcttatacttcctgtatatagcgcgtattattata	300
Db	241	gcgtatcagatggaanaactcgtggaagaattcttatacttcctgtatatagcgcgtattattata	300
QY	301	gggtgcggtgtgtgcctcaactaatgagatttaoaactcctacgtgaattggtttccagttta	360
Db	301	gggtgcggtgtgtgcctcaactaatgagatttaoaactcctacgtgaattggtttccagttta	360
QY	361	ggcattccttaagccacacatttgtttatgattcttaaaaaagattagataaagtattaaact	420
Db	361	ggcattccttaagccacacatttgtttatgattcttaaaaaagattagataaagtattaaact	420
QY	421	gtacaaaaaacgtataactgctattaaacccaattglatatgtgacagcaagaagtgtattat	480
Db	421	gtacaaaaaacgtataactgctattaaacccaattglatatgtgacagcaagaagtgtattat	480
QY	481	agaagttatcaatccatgagacaactttatlaaaaaaacctccacaagtttccaagga	540
Db	481	agaagttatcaatccatgagacaactttatlaaaaaaacctccacaagtttccaagga	540
QY	541	tcaagttttaaaactgtagaagtttaacgcgaagaacaaagtgtctctataatgaactct	600
Db	541	tcaagttttaaaactgtagaagtttaacgcgaagaacaaagtgtctctataatgaactct	600
QY	601	tcgggtttcaaacoggtttgcgaanaagttgtgaacttactctagaaaattgtgtcaactaga	660
Db	601	tcgggtttcaaacoggtttgcgaanaagttgtgaacttactctagaaaattgtgtcaactaga	660
QY	661	ttttctcaagctcagagatccaaattatgagaacccaagtttccacaggaacgcgcatttta	720
Db	661	ttttctcaagctcagagatccaaattatgagaacccaagtttccacaggaacgcgcatttta	720
QY	721	actgtatgcaatccatcatatgattttgttatgtttaaactattaggactctctaacttgt	780
Db	721	actgtatgcaatccatcatatgattttgttatgtttaaactattaggactctctaacttgt	780
QY	781	ggtttcgtattgtcaatgttlaaagaaatttgaagagaagactttttaaaaaacgtgcaa	840
Db	781	ggtttcgtattgtcaatgttlaaagaaatttgaagagaagactttttaaaaaacgtgcaa	840
QY	841	gattacaataatgtcaagcgttattctttgtaccagcaattggtttgcaattcttaataagaagt	900
Db	841	gattacaataatgtcaagcgttattctttgtaccagcaattggtttgcaattcttaataagaagt	900
QY	901	gaattactcgataaahatgatattatccaatttagttgaattgcatctcgtgcggaagact	960
Db	901	gaattactcgataaahatgatattatccaatttagttgaattgcatctcgtgcggaagact	960

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Db 901 gaattactcgataataatgatattatcaaatltagttgaaatgcatctgcygagcacct 960
Qy 961 ttatctaaagaatltgtgaagctgtgtgtaagcgttttaattaccgggtgtcttcaa 1020
Db 961 ttatctaaagaatltgtgaagctgtgtgtaagcgttttaattaccgggtgtcttcaa 1020
Qy 1021 ggcattgtgttacaagaacaacctctgcaattatatacacacgggaagcgatgataa 1080
Db 1021 ggcattgtgttacaagaacaacctctgcaattatatacacacgggaagcgatgataa 1080
Qy 1081 ccaggtgctctggcgaagtgtgtccattatattaagaacaaagtctgacttgat 1140
Db 1081 ccaggtgctctggcgaagtgtgtccattatattaagaacaaagtctgacttgat 1140
Qy 1141 aaaaacttggcccgacagacgttgagaagttgtgtgaaggtcctatgctatg 1200
Db 1141 aaaaacttggcccgacagacgttgagaagttgtgtgaaggtcctatgctatg 1200
Qy 1201 aaaggttatgtatgaataccagaagaacagaagaatcatagatgaagaagttgtg 1260
Db 1201 aaaggttatgtatgaataccagaagaacagaagaatcatagatgaagaagttgtg 1260
Qy 1261 cacaacggagatattggtgattacgaatgaagaaaaacattcttctatcgatcg 1320
Db 1261 cacaacggagatattggtgattacgaatgaagaaaaacattcttctatcgatcg 1320
Qy 1321 aagcttctaatcaatacaagaagatatacaccacccgtcgtaattagatctgtct 1380
Db 1321 aagcttctaatcaatacaagaagatatacaccacccgtcgtaattagatctgtct 1380
Qy 1381 ttgcaaacatcaaatatttttgatgcggcgctgtgtgcgttccagatccatagctgt 1440
Db 1381 ttgcaaacatcaaatatttttgatgcggcgctgtgtgcgttccagatccatagctgt 1440
Qy 1441 gagcttcgggagcgtgtgttctacttaagaagaagaatctatgatactgaagaagta 1500
Db 1441 gagcttcgggagcgtgtgttctacttaagaagaagaatctatgatactgaagaagta 1500
Qy 1501 atggaattcgtgtgtagtcaagtttcaaatgtcaaaacgtttgcgtgtgtgtccgttt 1560
Db 1501 atggaattcgtgtgtagtcaagtttcaaatgtcaaaacgtttgcgtgtgtgtccgttt 1560
Qy 1561 gtggcgaagatccctaaagttctcaatgttaaatgtgaaggttaagcaattagaagaata 1620
Db 1561 gtggcgaagatccctaaagttctcaatgttaaatgtgaaggttaagcaattagaagaata 1620
Qy 1621 ctgaagaaccagttgtcaagatg 1644
Db 1621 ctgaagaaccagttgtcaagatg 1644

RESULT 5
AA003257
ID AA003257 standard; DNA; 1644 BP.
XX
AC AA003257;
XX
DT 22-JUL-1990 (first entry)
XX
DE Luciola lateralis recombinant Luciferase gene.
XX
KW Luciferase; enzyme; ATP; plasmid pHL7; firefly; ss.
XX
OS Luciola lateralis.
XX
FH Key 1..1644
FT CDS 1..1644
FT /*tag= a
FT /product=Luciferase
FT /EC_number=EC-1.13.12.7
XX
XX EP353464-A.
XX
5
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PD 07-FEB-1990.
XX
PF 30-JUN-1989; 89EP-0111958.
XX
PR 22-DEC-1988; 88JP-0162402.
PR 01-JUL-1988; 88JP-0162402.
XX
PA (KIKK ) KIKKOMAN CORP.
XX
PI Tatsumi H, Kaiiyama N, Nakano E;
XX WPI; 1990-038240/06.
DR P-PSDB; AAR03731.
XX
PT New gene encoding luciferase -
PT derived from Luciola lateralis and expressed in and purified
PT from Escherichia coli genus cells.
XX
XX Claim 3; page 24; 43pp; English.
CC This enzyme is useful for determining ATP levels. It is
CC contained in plasmid pHL7.
XX
SQ Sequence 1644 BP; 529 A; 264 C; 348 G; 503 T; 0 other;

Query Match 99.3%; Score 1632.8; DB 11; Length 1644;
Best Local Similarly 99.6%; Pred. No. 0;
Matches 1637; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 atggaanaacatggaagacatgaanaatattgtgtatgctgcctgaaccattaccctatt 60
Db 1 atggaanaacatggaagacatgaanaatattgtgtatgctgcctgaaccattaccctatt 60
Qy 61 gaagagagatcgtctgagacacattgcgcaagtataatgatcgaatagacaaacttga 120
Db 61 gaagagagatcgtctgagacacattgcgcaagtataatgatcgaatagacaaacttga 120
Qy 121 gaattgcttttaactaagcacttaacgggtgtcgtatagcgtacgacgaatacttaga 180
Db 121 gaattgcttttaactaagcacttaacgggtgtcgtatagcgtacgacgaatacttaga 180
Qy 181 aatcatcgtctctagaggaagccttaagaactatggtttgtgtatggaagaact 240
Db 181 aatcatcgtctctagaggaagccttaagaactatggtttgtgtatggaagaact 240
Qy 241 ggcattatcagtggaataactcttattctctgtattagccggttattata 300
Db 241 ggcattatcagtggaataactcttattctctgtattagccggttattata 300
Qy 301 ggtgcgtgtgtgtccaaactaataagatttaccctcagcgtgaattgtacagttta 360
Db 301 ggtgcgtgtgtgtgtccaaactaataagatttaccctcagcgtgaattgtacagttta 360
Qy 361 ggcattctaaagccaacattgtatttagttttaaanaaggaattagataaacttaact 420
Db 361 ggcattctaaagccaacattgtatttagttttaaanaaggaattagataaacttaact 420
Qy 421 gtacaaaaaagcgtatcgtctatataaacacattgttatatttgacagcaagtgtat 480
Db 421 gtacaaaaaagcgtatcgtctatataaacacattgttatatttgacagcaagtgtat 480
Qy 481 agaggttatcaatcagtagcaacttataaaaaaacaccccaaggtttcaagga 540
Db 481 agaggttatcaatcagtagcaacttataaaaaaacaccccaaggtttcaagga 540
Qy 541 tcaagtttaaacctgttagaagttacacgcaagaacagttgctctataatgaactct 600
Db 541 tcaagtttaaacctgttagaagttacacgcaagaacagttgctctataatgaactct 600
Qy 601 tcgggttcaacccgtttgcgaagaaggtgtgcaacttactcatgaaattgtgactaga 660
Db 601 tcgggttcaacccgtttgcgaagaaggtgtgcaacttactcatgaaattgtgactaga 660
```

QY	661	ttttctacgcttagagataccaatttaiggaaccaaagtttcaacgaagcgagctattta	720
Db	661	ttttctacgcttagagataccaatttaiggaaccaaagtttcaacgaagcgagctattta	720
QY	721	actgtatgacatctcatcatggtttgtgtatgatttactactttaggtgcatactatgt	780
Db	721	actgtatgacatctcatcatggtttgtgtatgatttactactttaggtgcatactatgt	780
QY	781	ggtttcggtatctgcatgtttaacgaaatttgacgaagagactttttaaaacacgtgca	840
Db	781	ggtttcggtatctgcatgtttaacgaaatttgacgaagagactttttaaaacacgtgca	840
QY	841	gatttaacaaagttccaagcggtatctctgttgcacgacttctgttgcaattcttaataag	900
Db	841	gatttaacaaagttccaagcggtatctctgttgcacgacttctgttgcaattcttaataag	900
QY	901	gaattactcgtataataatgatttatccaatttgaattgaaatgtgcatctcgcgagcaact	960
Db	901	gaattactcgtataataatgatttatccaatttgaattgaaatgtgcatctcgcgagcaact	960
QY	961	ttatctaaagaaattgtgtgaagctgttgcctagaagtttataattgacggtgttcgtcca	1020
Db	961	ttatctaaagaaattgtgtgaagctgttgcctagaagtttataattgacggtgttcgtcca	1020
QY	1021	ggctatggtttaacaanaaacctctgaattatataccaacgggaagcgatgatgaa	1080
Db	1021	ggctatggtttaacaanaaacctctgaattatataccaacgggaagcgatgatgaa	1080
QY	1081	ccaggtgctctcgcgaaagttgtgcacattatttaagcaaaaagttatcgacttgatact	1140
Db	1081	ccaggtgctctcgcgaaagttgtgcacattatttaagcaaaaagttatcgacttgatact	1140
QY	1141	aaaaaaccttggcccggaacagcttgagaagtttggtaaaaggtccatgctatg	1200
Db	1141	aaaaaaccttggcccggaacagcttgagaagtttggtaaaaggtccatgctatg	1200
QY	1201	aaaggtcatgtagaataccaagaagaacaagaatcatatgaaagaaagttgtgtg	1260
Db	1201	aaaggtcatgtagaataccaagaagaacaagaatcatatgaaagaaagttgtgtg	1260
QY	1261	cacacagagagatatgtgtgatactacgatgagaanaaacattcttatactcggtgactgtg	1320
Db	1261	cacacagagagatatgtgtgatactacgatgagaanaaacattcttatactcggtgactgtg	1320
QY	1321	aagctttaatcaaatcaaaagatactgaagtacacacccgtcggaattgaatcctgttct	1380
Db	1321	aagctttaatcaaatcaaaagatactgaagtacacacccgtcggaattgaatcctgttct	1380
QY	1381	ttgacaatccaaatatcttttctgtgcgcgcgtgtgcgtgcgtccagatccatagtcgt	1440
Db	1381	ttgacaatccaaatatcttttctgtgcgcgcgtgtgcgtgcgtccagatccatagtcgt	1440
QY	1441	gagcttccggagagctgtgtgttgaacttaagaaagaaatctaagactgaaaaaaga	1500
Db	1441	gagcttccggagagctgtgtgttgaacttaagaaagaaatctaagactgaaaaaaga	1500
QY	1501	atgagtaacgttgtatgatacagttccaagtccaagtcgaaacggttcgtgtgtgtccggtt	1560
Db	1501	atgagtaacgttgtatgatacagttccaagtccaagtcgaaacggttcgtgtgtgtccggtt	1560
QY	1561	gttgagcgaagtaaccataaagtlctcaactgtgtaaaattgacggtataagcaattagaga	1620
Db	1561	gttgagcgaagtaaccataaagtlctcaactgtgtaaaattgacggtataagcaattagaga	1620
QY	1621	ctggaagaacacagtttgttaagatg	1644
Db	1621	ctggaagaacacagtttgttaagatg	1644

XX	AA663269;	
XX		
DT	20-MAY-1997	(first entry)
DE	Gene for firefly luciferase conjugated with 87 aa peptide at 3' end.	
KW	Fusion protein; firefly; Luciola lateralis; luciferase; biotinylation;	
KW	wild type; E.coli; bioluminescence assay; quantification; ligand;	
KW	receptor; ds.	
XX		
OS	Synthetic.	
XX		
PH	Key	Location/Qualifiers
FT	CDS	1..1641
FT		/*tag= a
FT		/note= "encodes firefly portion of fusion protein"
FT	CDS	1642..1647
FT		/*tag= b
FT		/note= "sequence encoded by linker used to insert
FT		sequence encoding biotin peptide to generate
FT		fusion gene"
FT	CDS	1648..1908
FT		/*tag= C
FT		/note= "encodes biotinylated peptide portion of fusion
XX		protein"
PN	JP08308578-A.	
PD	26-NOV-1996.	
XX		
XX	24-APR-1995;	95JP-0098857.
PF		
XX	14-MAR-1995;	95JP-0054625.
PR		
XX	27-JUL-1994;	94JP-0193798.
XX		
PA	(KIKK) KIKKOMAN CORP.	
XX		
DR	WPI: 1997-059697/06.	
XX	P-PSDB; AAMI2395.	
XX		
PT	Fusion protein comprising firefly luciferase and biotinylated	
PT	peptide - useful in a bio-luminescent analytical method for	
PT	quantifying ligands	
XX		
PS	Example 7, Page 11-12; 13pp; Japanese.	
XX		
CC	This is the nucleotide sequence encoding a novel fusion protein which	
CC	comprises the firefly (Luciola lateralis) luciferase protein and an 87	
CC	amino acid biotinylated peptide designated the E.coli biotin carboxy	
CC	carrier protein (BCCP-87). The fusion gene was generated by firstly	
CC	amplifying the sequence encoding the E.coli (BCCP-87) from the E.coli	
CC	genome and inserting the resultant sequence into the 3' end of the	
CC	firefly luciferase gene in plasmid pHlF30. The biotin peptide sequence	
CC	replaces the C-terminal Met residue of the wild type luciferase sequence.	
CC	The plasmid was then introduced into E.coli JM101 for production of the	
CC	fusion protein. The novel protein can be used in bioluminescence assays	
CC	to quantify luciferase ligands which may modulate binding of luciferase	
CC	to its receptor.	
XX		
Sequence	1908 BP; 598 A; 329 C; 426 G; 555 T; 0 other;	

RESULT	6
AAT63269	
ID	AAT63269 standard; DNA; 1908 BP

Query Match	Best Local Similarity	Score 1631.4	DB 18	Length 1908
Matches 1635; Conservative	99.2%;	Pred. No. 0;	Indels 6;	Gaps 0
Qy	1 atggaacacatgagagacatgtaaatatctgtgtatagtcgcgcgaacacatttaccctatt	60		
Db	1 atggaacacatgagagacatgtaaatatctgtgtatagtcgcgcgaacacatttaccctatt	60		
Qy	61 gaagagcatctgctgtagacacaaattgcgcgaagtatatagatcgcataatgcaaaccttga	120		

Dh 61 gaagaggatctgctgagcacaattgcgcaatatagtatcgatatctgcaaaattgga 120
Qy 121 gcaattgctttaaatacgaactacgcggtgctgattatatacgtacgcgcaatactaa 180
Dh 121 gcaattgctttaaatacgaactacgcggtgctgattatatacgtacgcgcaatactaa 180
Qy 181 aaatactgcttctagagagagccttaagaataatggttggctgtgtgtaagaaat 240
Dh 181 aaatactgcttctagagagagccttaagaataatggttggctgtgtgtaagaaat 240
Qy 241 gcttatgcaatgaaactgaaactgtgaacttcttcttcttcttcttcttcttcttctt 300
Dh 241 gcttatgcaatgaaactgaaactgtgaacttcttcttcttcttcttcttcttcttctt 300
Qy 301 ggttcggtgtgctgcaactaaatgagattacacttaacgtatgcaatggttcaagttta 360
Dh 301 ggttcggtgtgctgcaactaaatgagattacacttaacgtatgcaatggttcaagttta 360
Qy 361 ggcattcttaagcacaacttcttatttcttcttcttcttcttcttcttcttcttctt 420
Dh 361 ggcattcttaagcacaacttcttatttcttcttcttcttcttcttcttcttcttctt 420
Qy 421 gtaacaaaacggttaactgctatataaacattgttatatttgacgcgcaaatggtattat 480
Dh 421 gtaacaaaacggttaactgctatataaacattgttatatttgacgcgcaaatggtattat 480
Qy 481 agaggttatcaatcgaatggaacttataaaacacacacacacacacacacacacacacac 540
Dh 481 agaggttatcaatcgaatggaacttataaaacacacacacacacacacacacacacacac 540
Qy 541 taaagtttaaaactgttgaagtttaacccgaagaacaggttgccttataatgaactct 600
Dh 541 taaagtttaaaactgttgaagtttaacccgaagaacaggttgccttataatgaactct 600
Qy 601 tcgggttcaacggttgcgcaaaaggtgtgcaacttaccatgaataaatttgcctactaga 660
Dh 601 tcgggttcaacggttgcgcaaaaggtgtgcaacttaccatgaataaatttgcctactaga 660
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Dh 661 tttcttcacgctagagatcccaatttataggaaacaaagttccacacgacgcgtatttta 720
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Dh 721 actgtagtaccattccatcatatggttggtagtttactactttaggctatctacttgt 780
Qy 781 ggtttcgtatgtcactgcttaacgaatgtgaagagagactttttaaaacacgca 840
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Dh 841 gattacaatgttcaagcgttatcttctgtacgcgacttgttgcgaatttcttaataagaat 900
Qy 901 gaattactgataaataatgattatcaaatattagttgaattgcatctgcgagagacact 960
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Qy 961 ttatctaaagaatgttgaagcgttgcctgtagacgttcttaatttaccggtgtgtcga 1020
Dh 961 ttatctaaagaatgttgaagcgttgcctgtagacgttcttaatttaccggtgtgtcga 1020
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Dh 1021 ggcctatggtttaacagaacacactctgcaattatatacaccggaagcgatgataa 1080
Qy 1081 caaggtgcttctgcaaaagttgtgcattatttaagcaaaagttatcgatcttgatact 1140
Dh 1081 caaggtgcttctgcaaaagttgtgcattatttaagcaaaagttatcgatcttgatact 1140
Qy 1141 aaaaaaacttggccgcaacagacgttgagagaagtttgtaaaaggttccatgtgcttacy 1200
Dh 1141 aaaaaaacttggccgcaacagacgttgagagaagtttgtaaaaggttccatgtgcttacy 1200

Qy 1201 aaagttatgtagataatccagaagcacagaagaatactatagatgaagaagttgttg 1260
Dh 1201 aaagttatgtagataatccagaagcacagaagaatactatagatgaagaagttgttg 1260
Qy 1261 cacacaagagatatgttgatatacgaatgaagaacacattcttatacgtgacgttg 1320
Dh 1261 cacacaagagatatgttgatatacgaatgaagaacacattcttatacgtgacgttg 1320
Qy 1321 aagcttttaatacaataaagaagatatcaagtccaccctgtgaatgaatactgttct 1380
Dh 1321 aagcttttaatacaataaagaagatatcaagtccaccctgtgaatgaatactgttct 1380
Qy 1381 ttgcaacatcaaatatttttgatgcccgcgtgtgctgcttccagaatccataagctgt 1440
Dh 1381 ttgcaacatcaaatatttttgatgcccgcgtgtgctgcttccagaatccataagctgt 1440
Qy 1441 gaagcttcggagagcgtgtgtgtacttaagaagaacacacacacacacacacacacacacac 1500
Dh 1441 gaagcttcggagagcgtgtgtgtacttaagaagaacacacacacacacacacacacacacac 1500
Qy 1501 atgattacgttgcctgacgaatttcaaatgcaaaacggttgcgtgtgtgtgtgtgtgtgt 1560
Dh 1501 atgattacgttgcctgacgaatttcaaatgcaaaacggttgcgtgtgtgtgtgtgtgtgt 1560
Qy 1561 gtgacgaagttacaaagttcctacgtgtaaatgtgacgtgataaagcaattagaagaata 1620
Dh 1561 gtgacgaagttacaaagttcctacgtgtaaatgtgacgtgataaagcaattagaagaata 1620
Qy 1621 ctgaagaacacagttgctaag 1641
Dh 1621 ctgaagaacacagttgctaag 1641
RESULT 7
AAV32467 standard; DNA; 1920 BP.
ID AAV32467
XX
AC AAV32467;
XX
XX 10-SEP-1998 (first entry)
Dh
XX Luciferase-lysostaphin fused gene.
DE Luciferase-lysostaphin fused gene.
XX
XX Luciferase-lysostaphin fused gene; chimeric; bioluminescence; ds.
KW Chimeric - Staphylococcus simulans.
XX Chimeric - Luciola lateralis.
OS
OS Chimeric - Staphylococcus simulans.
OS
FH Key
FT CDS
FT 1..1920
FT /tag= a
FT /product= "Luciferase-lysostaphin fusion protein"
FT /note= "Nucleotides 1-1647 encode luciferase
FT protein while nucleotides 1648-1920 encode
FT lysostaphin; CDS does not contain stop codon"
PN JP10150991-A.
XX
XX 09-JUN-1998.
PD
XX 25-NOV-1996; 96JP-0328042.
PF
XX 25-NOV-1996; 96JP-0328042.
PR
XX 25-NOV-1996; 96JP-0328042.
XX
PA (KIKK) KIKKOMAN CORP.
XX
XX WPI: 1998-379994/33.
DR
XX P-PSDB: AAM48856.
XX
XX
PT New Luciferase-lysostaphin fused protein - useful for
XX bioluminescence analysis

PS Disclosure; Pages 6-7; 10pp; Japanese.

CC The invention claims for a luciferase-lyso-staphin fused gene which
CC encodes a fused protein in which a peptide part consisting of
CC luciferase, from *Luciola lateralis*, is connected to a peptide part
CC consisting of lyso-staphin from *Staphylococcus simulans*. The method
CC described by the invention can be used to prepare a luciferase-
CC lyso-staphin fused protein efficiently. The fused protein is useful
CC for bioluminescence analysis.

XX Sequence 1920 BP; 627 A; 310 C; 407 G; 576 T; 0 other;

Query Match

Best Local Similarity 99.2%; Score 1631.4; DB 19; Length 1920;

Matches 1635; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 atggaanaacatgagagacatgaaataattgtatgtgtcctgaacatttaccctat 60
Db 1 atggaanaacatgagagacatgaaataattgtatgtgtcctgaacatttaccctat 60
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Db 61 gaaaggagatctgtcgtggagacaaattgtcgcaagtataatgataatgcaaaacttga 120
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Db 121 gcaattgtcttactaacgcaactacccgtgtcgatataacgtaacggaataacttaaa 180
Qy 181 aatcatgtctgtctagagagagctttaaagaattatgtgtgtgtgtatgaaagaatt 240
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Db 241 ggcattatgagagaaacgttgaagaattcttaccgtatgtaacgggttatatta 300
Qy 301 ggtgtcgtgtgtgtcctcaactaatatagatttcaactctacgtgaattgttcaacgttta 360
Db 301 ggtgtcgtgtgtgtcctcaactaatatagatttcaactctacgtgaattgttcaacgttta 360
Qy 361 ggcattctcaagccaacattgtattagttcttaaaagaattagataaagttaact 420
Db 361 ggcattctcaagccaacattgtattagttcttaaaagaattagataaagttaact 420
Qy 421 gtaacaaaacggtactgtctatataaacattgttatattggaagcaaaagttaatt 480
Db 421 gtaacaaaacggtactgtctatataaacattgttatattggaagcaaaagttaatt 480
Qy 481 agaggttatcaatccatgacacactttataaaaaaaccccaaggtttcaaaaga 540
Db 481 agaggttatcaatccatgacacactttataaaaaaaccccaaggtttcaaaaga 540
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Db 601 tccgggttcaacccggtttgccaagaaggtgtgcaacttaccacgaagaatttgcgcgct 660
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Db 661 ttttctcaacgttagatccaaattataggaacaaagtttcaacggcagcgtatatta 720
Qy 721 actgtatgataccatccatcatatgtgtgtgttactacttgggtacttaactgtg 780
Db 721 actgtatgataccatccatcatatgtgtgtgttactacttgggtacttaactgtg 780
Qy 781 ggttttcgattgtatgtttaaagaaatttgaagaaagactttttaaacaacttgaa 840
Db 781 ggttttcgattgtatgtttaaagaaatttgaagaaagactttttaaacaacttgaa 840

Qy 841 gattacaatgttcaacggttatctgttaccgacttgttgcgaattcttaataagaagt 900
Db 841 gattacaatgttcaacggttatctgttaccgacttgttgcgaattcttaataagaagt 900
Qy 901 gaattactgataataatgatattatcaaatattagttgaattgtcatctgcgagacact 960
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Qy 961 ttattcaagaagaattgttgaagctgtgtctgtagaagtttaatttaccgggtgttcgtcaa 1020
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Qy 1021 ggcatagtttaacagagaacacactctgcaattatataccacggaaggcgtatgaata 1080
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Qy 1141 aaaaaaactttggcccgaaacagacgtggaagttgtgttaaagggttccatgtatg 1200
Db 1141 aaaaaaactttggcccgaaacagacgtggaagttgtgttaaagggttccatgtatg 1200
Qy 1201 aaaggttatgtagaataatccagaagcaacagagaataatcaatagatgaagaagttggttg 1260
Db 1201 aaaggttatgtagaataatccagaagcaacagagaataatcaatagatgaagaagttggttg 1260
Qy 1261 cacaacagagatatttgggtatccagatgaagaataaacattcttaccgtgagctgttg 1320
Db 1261 cacaacagagatatttgggtatccagatgaagaataaacattcttaccgtgagctgttg 1320
Qy 1321 aagctttaaatacaatacaaaagatatacaagttacacactctgtaattagatctgttct 1380
Db 1321 aagctttaaatacaatacaaaagatatacaagttacacactctgtaattagatctgttct 1380
Qy 1381 ttgcaacatccaaatattttgtatgtccggtgtgtgtgtccagatccataagctgtg 1440
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Qy 1441 gagcttccggagagctgt 1500
Db 1441 gagcttccggagagctgt 1500
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Db 1501 atgattacgttgcgtgacaggttcaaatgtcaaacgtttgcgtgtgtgtgtgtgtgtgt 1560
Qy 1561 gtgagcgaagttacactaaagtgtctactgttgaataatgacggttaagaagaata 1620
Db 1561 gtgagcgaagttacactaaagtgtctactgttgaataatgacggttaagaagaata 1620
Qy 1621 ctgaagaacacagttgtctaag 1641
Db 1621 ctgaagaacacagttgtctaag 1641

RESULT 8

AAT33850
ID AAT33850 standard; DNA; 2019 BP.

AC AAT33850;

DT 12-NOV-1996 (first entry)

DE DNA encoding streptavidin/luciferase fusion protein.

KW Streptavidin; luciferase; fusion protein;

KW Streptomyces avidinii; *Luciola lateralis*; firefly;

KW recombinant production; industry; ds.
OS Synthetic.

|||||
Db 2004 accagttgctaagatg 2019
RESULT 9
ID AAT33851 standard; DNA: 2055 BP.
XX AAT33851:
AC AAT33851:
XX 12-NOV-1996 (first entry)
XX DNA encoding mutant streptavidin/Luciferase fusion protein.
XX
XX
XX Mutant: streptavidin: luciferase: fusion protein:
XX Streptomyces avidinii; Luciola lateralis; firefly;
XX recombinant production; Industry; ds.
XX
XX Synthetic.
XX
XX Key location/Qualifiers
FT CDS 1..2055 a
FT /tag- a
FT /note- "STOP codon absent"
XX
XX JP07289264-A.
XX
XX 07-NOV-1995.
XX
XX 27-APR-1994; 94JP-0090275.
XX
XX 27-APR-1994; 94JP-0090275.
XX
XX (KIKK) KIKKOMAN CORP.
XX
XX WPI; 1996-015269/02.
XX P-PSDB; AAM04208.
XX
XX
XX New mutant streptavidin (SA) gene - fused to a firefly luciferase
XX gene, for the recombinant prepn. of a SA-FL fused protein
XX
XX
XX Claim 1; Pages 7-8; 12pp; Japanese.
XX
XX
XX The present sequence encodes a mutant streptavidin/Luciferase
XX fusion protein, comprising a mutant Streptomyces avidinii
XX streptavidin gene and the Luciola lateralis (firefly) luciferase
XX gene. The fusion protein can be prepd. by inserting the
XX recombinant DNA encoding it into a Escherichia species microbe,
XX culturing the transformed microbe in a medium and collecting the
XX fusion protein from the culture. The fusion protein can be used
XX in industry.
XX
XX
XX Sequence 2055 BP; 603 A; 418 C; 474 G; 560 T; 0 other:
SQ
Query Match 98.7%; Score 1623.2; DB 17; Length 2055;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1628; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 600 ctgtctaggagagcgtttaagaatattggttgggttgatggaagtgcgtatg 659
Qy 249 caatgaaactgtgaagaattcttattctcgtattactgacgggttattataggttcg 308
Db 660 cagtgaaactgtgaagaattcttattctcgtattactgacgggttattataggttcg 719
Qy 309 tgtgtcccaactaattgaatttacaactcgtgaattgtgttcacagtttaggcattc 368
Db 720 tgtgtcccaactaattgaatttacaactcgtgaattgtgttcacagtttaggcattc 779
Qy 369 taagccaactatgtattttagttcttaaaaaagattatagataagtttaactgtcaaaa 428
Db 780 taagccaactatgtattttagttcttaaaaaagattatagataagtttaactgtcaaaa 839
Qy 429 aacggttaactgtattttagttcttaaaaaagattatagataagttttagaggtta 488
Db 840 aacggttaactgtattttagttcttaaaaaagattatagataagttttagaggtta 899
Qy 489 tcaatccatgacaaacttatttaaaaaaacactccacaagtttccaagaagttcaagtt 548
Db 900 tcaatccatgacaaacttatttaaaaaaacactccacaagtttccaagaagttcaagtt 959
Qy 549 taaactgtagaagtttaaccgcaagaagaagttgtcttataatgaactcttggttc 608
Db 960 taaactgtagaagtttaaccgcaagaagaagttgtcttataatgaactcttggttc 1019
Qy 609 aaccggttggccaaaaggtgtgaacttaactcaatgaataattgtcaactatcttca 668
Db 1020 aaccggttggccaaaaggtgtgaacttaactcaatgaataattgtcaactatcttca 1079
Qy 669 cgtctagatgccaatattatggaataccaagtttccaccagcagcgtattttagctgtagt 728
Db 1080 cgtctagatgccaatattatggaataccaagtttccaccagcagcgtattttagctgtagt 1139
Qy 729 accattccatcaggtttgttattgttactactttaggtattactgtgtgtttg 788
Db 1140 accattccatcaggtttgttattgttactactttaggtattactgtgtgtttg 1199
Qy 789 tattgtcatgttaacgaataattgacgaagaagactttttaaaaaactccaagattaca 848
Db 1200 tattgtcatgttaacgaataattgacgaagaagactttttaaaaaactccaagattaca 1259
Qy 849 atgtccaagcttattctgttaccgaactgtttgtcaattcttaataagaagttaact 908
Db 1260 atgtccaagcttattctgttaccgaactgtttgtcaattcttaataagaagttaact 1319
Qy 909 cgataataatgattatcaaatattgaattgacatctgtgagggacacttattactaa 968
Db 1320 cgataataatgattatcaaatattgaattgacatctgtgagggacacttattactaa 1379
Qy 969 agaatgtgtgaagcgtgtgtgacggttttaattaccgggtgtgtcgtcaaggctatg 1028
Db 1380 agaatgtgtgaagcgtgtgtgacggttttaattaccgggtgtgtcgtcaaggctatg 1439
Qy 1029 tttaacagaacaacactctgcaatttattacacacgggaaggcagatgaacagggtgc 1088
Db 1440 tttaacagaacaacactctgcaatttattacacacgggaaggcagatgaacagggtgc 1499
Qy 1089 ttctgtgcaaaagtgtgtccattattaaagcaaaagtatccgactgtgaactaaaaaac 1148
Db 1500 ttctgtgcaaaagtgtgtccattattaaagcaaaagtatccgactgtgaactaaaaaac 1559
Qy 1149 ttgtggccggaagaagcgtgtgaagaattgtgtgaagggtccctatgtatgaagaagtt 1208
Db 1560 ttgtggccggaagaagcgtgtgaagaattgtgtgaagggtccctatgtatgaagaagtt 1619
Qy 1209 tgtatgaataccagaagcaagaagataatcatatagaatgaagaagttgtgtcacacag 1268
Db 1620 tgtatgaataccagaagcaagaagataatcatatagaatgaagaagttgtgtcacacag 1679
Qy 1269 agatattgggtattacgaatgaagaataaactcttattacgtgtgactgttgaggtctt 1328
Db 1680 agatattgggtattacgaatgaagaataaactcttattacgtgtgactgttgaggtctt 1739

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QY 1329 aatcaatacaagaatcatcaagttaccactgtgtaattagaatctgttcttttgcacaa 1388
DB 1740 aatcaatacaagaatcatcaagttaccactgtgtaattagaatctgttcttttgcacaa 1799
QY 1389 tccaaatatttttgatgctgcgcgttctgtgctgtccagatctatagctgtgtgagcttcc 1448
DB 1800 tccaaatatttttgatgctgcgcgttctgtgctgtccagatctatagctgtgtgagcttcc 1859
QY 1449 gggagctgtgtgttacttaagaagaataatctatgactgtaaaaaagaagttaagtta 1508
DB 1860 gggagctgtgtgttacttaagaagaataatctatgactgtaaaaaagaagttaagtta 1919
QY 1509 cgttgctagtcgaagtttcaaatgcaaaacgtttgctgtgtgtgtccgttttttgagca 1568
DB 1920 cgttgctagtcgaagtttcaaatgcaaaacgtttgctgtgtgtgtccgttttttgagca 1979
QY 1569 agtacctaaaggtctcaactgtgtaaaaattgacggttaagaacattagaagaatactaga 1628
DB 1980 agtacctaaaggtctcaactgtgtaaaaattgacggttaagaacattagaagaatactaga 2039
QY 1629 accagttgcttaagt 1644
DB 2040 accagttgcttaagt 2055

RESULT 10
AAT63268
ID AAT63268 standard; DNA; 1704 BP.
XX
AC AAT63268;
XX
DT 20-MAY-1997 (first entry)
XX
DE Firefly Luciferase conjugated with 23 aa peptide at 5' end.
XX
KW Fusion protein; firefly; luciola lateralis; luciferase; biotinylation;
KW wild type; E.coli; bioluminescence assay; quantification; ligand;
KW receptor; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 1..75
FT CDS /note= "encodes biotinylated peptide"
FT 76..1704
FT /tag= b
FT /note= "encodes firefly luciferase residues 4-54"
XX
FN JP08308578-A.
XX
PD 26-NOV-1996.
XX
PF 24-APR-1995; 95JP-0098857.
XX
PR 14-MAR-1995; 95JP-0054625.
XX
PR 27-JUL-1994; 94JP-0193798.
XX
PA (RIKK ) KIKKOMAN CORP.
XX
DR WPI; 1997-059697/06.
DR P-PSDB; AAMI2394.
XX
XX Fusion protein comprising firefly luciferase and biotinylated
XX peptide - useful in a bio-luminescent analytical method for
XX quantifying ligands
XX
PS Example 1; Page 9-10; 13pp; Japanese.
XX
CC This is the nucleotide sequence encoding a novel fusion protein which
CC comprises the firefly (luciola lateralis) luciferase protein and a
CC 23 amino acid biotinylated peptide designated Biotin peptide #84.

```

CC The gene was generated by firstly annealing the sequence encoding
 CC peptide #84 (AAT63270) and its complementary sequence, then inserting the
 CC resultant double stranded sequence into the 5' end of the luciferase gene
 CC in plasmid pHL108. The biotin peptide sequence replaces the first 4
 CC amino acids of the wild type luciferase sequence. The plasmid was then
 CC introduced into E.coli JM101 for production of the fusion protein. The
 CC novel protein can be used in bioluminescence assays to quantify
 CC luciferase ligands which may modulate binding of luciferase to its
 CC receptor.
 CC
 SQ Sequence 1704 BP; 541 A; 275 C; 361 G; 527 T; 0 other;

Query Match 98.7%; Score 1622.8; DB 18; Length 1704;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1627; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 11 tggagaacgatgaaatattgtgtatgctcctgaaccatttaccctatgaagagat 70
DB 71 tggagaacgatgaaatattgtgtatgctcctgaaccatttaccctatgaagagat 130
QY 71 ctgctggagcacaattgacgaagatatagtatcgatatacgaaaacttggagcaattgctt 130
DB 131 ctgctggagcacaattgacgaagatatagtatcgatatacgaaaacttggagcaattgctt 190
QY 131 ttactaacgacttaccggtgttcgattatagctgacgacgaatttgaagaatactatgct 190
DB 191 ttactaacgacttaccggtgttcgattatagctgacgacgaatttgaagaatactatgct 250
QY 191 gcttagaagagcgttaagaattatgcttctgtgtgtgtatgaagaattgcttga 250
DB 251 gcttagaagagcgttaagaattatgcttctgtgtgtgtatgaagaattgcttga 310
QY 251 gttgaaacgttgaagaatttcttctgtgtgtgtatgaagaattgcttga 310
DB 311 gttgaaacgttgaagaatttcttctgtgtgtgtatgaagaattgcttga 370
QY 311 tggctccaactatgagatttcaactcctagctgaatttggccaagtttagcactcta 370
DB 371 tggctccaactatgagatttcaactcctagctgaatttggccaagtttagcactcta 430
QY 371 agccaacaattgatttagttcttaaaaaagattagataaagttataactgtatacaaaaa 430
DB 431 agccaacaattgatttagttcttaaaaaagattagataaagttataactgtatacaaaaa 490
QY 431 cggtaactgtcttaaaacctgttataattgaaagcaaatgtattataggtttacc 490
DB 491 cggtaactgtcttaaaacctgttataattgaaagcaaatgtattataggtttacc 550
QY 491 aatcatggacaactttataaaaaaacactccacaaggtttcaaaagatcaattta 550
DB 551 aatcatggacaactttataaaaaaacactccacaaggtttcaaaagatcaattta 610
QY 551 aaactgtagaattacccgcaagaagaacagttgtcttataatgaacttccgggttcaa 610
DB 611 aaactgtagaattacccgcaagaagaacagttgtcttataatgaacttccgggttcaa 670
QY 611 ccggtttgccaagaaggtgacgaacttaccatgaaatattgttccatgattttccag 670
DB 671 ccggtttgccaagaaggtgacgaacttaccatgaaatattgttccatgattttccag 730
QY 671 cttagatcccaatttatggaaacaaagtttccacggcgacgcttatttaactgtatgac 730
DB 731 cttagatcccaatttatggaaacaaagtttccacggcgacgcttatttaactgtatgac 790
QY 731 catccatcatggtttgtgtatgttactactttaggctatacttaactgtgttgcgta 790
DB 791 catccatcatggtttgtgtatgttactactttaggctatacttaactgtgttgcgta 850
QY 791 ttgtatgttaacgaatttgcgaagagactttttaaaccactgcgaagttacaat 850
DB 851 ttgtatgttaacgaatttgcgaagagactttttaaaccactgcgaagttacaat 910

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QY 851 gtcaagcgtatctctgtaccgacttgttgcgaattcttaataagatgaattactcg 910
 DB 911 gtcaagcgtatctctgtaccgacttgttgcgaattcttaataagatgaattactcg 970
 QY 911 ataaatgatcttcaaatgaattgaatctgacatctgacgagacacttatactaaag 970
 DB 971 ataaatgatcttcaaatgaattgaatctgacatctgacgagacacttatactaaag 1030
 QY 971 aaattgtgaaagcgtgtgtctagaagcttttaattaccggggtgttcgccaagagctatgct 1030
 DB 1031 aaattgtgaaagcgtgtgtctagaagcttttaattaccggggtgttcgccaagagctatgct 1090
 QY 1031 taacagaacaacactctgcgaattatcaacacggaagcgatgaataaacaagtgctc 1090
 DB 1091 taacagaacaacactctgcgaattatcaacacggaagcgatgaataaacaagtgctc 1150
 QY 1091 ctggaagaagtggtccattatcttaagaacaaagtatcgatcttgatactaaacaaact 1150
 DB 1151 ctggaagaagtggtccattatcttaagaacaaagtatcgatcttgatactaaacaaact 1210
 QY 1151 tgggcccgaacagacgtggaagaagttgtgaaagggtccattatcttaagaagaagtgatg 1210
 DB 1211 tgggcccgaacagacgtggaagaagttgtgaaagggtccattatcttaagaagaagtgatg 1270
 QY 1211 tagataatccagagaacaaagagaatcatagatgaagaagtggtgtgacacagagag 1270
 DB 1271 tagataatccagagaacaaagagaatcatagatgaagaagtggtgtgacacagagag 1330
 QY 1271 atattggatcatcagatgaagaacaaacattcttalcgtgagatcgtttgaagtccttaa 1330
 DB 1331 atattggatcatcagatgaagaacaaacattcttalcgtgagatcgtttgaagtccttaa 1390
 QY 1331 tcaaatataaaggatataaagatcacactgctgaattagaatcgttcttctttgaaacatc 1390
 DB 1391 tcaaatataaaggatataaagatcacactgctgaattagaatcgttcttctttgaaacatc 1450
 QY 1391 caaatatttgcagtcgagcgttgcgttgcacatccatagctgtaagcttcacg 1450
 DB 1451 caaatatttgcagtcgagcgttgcgttgcacatccatagctgtaagcttcacg 1510
 QY 1451 gaggctgtgtgtacttaagaagaacaaactctatgactgaagaagaagtaagtactaa 1510
 DB 1511 gaggctgtgtgtacttaagaagaacaaactctatgactgaagaagaagtaagtactaa 1570
 QY 1511 ttgctagtcgaagttccaatgcaaaacgcttgcgtggtggtgcgttcttcttgaagagag 1570
 DB 1571 ttgctagtcgaagttccaatgcaaaacgcttgcgtggtggtgcgttcttcttgaagagag 1630
 QY 1571 taacctaaagtcctcactgttaaatgtgacggtlaaagcaactagagaatactctgaagaac 1630
 DB 1631 taacctaaagtcctcactgttaaatgtgacggtlaaagcaactagagaatactctgaagaac 1690
 QY 1631 cagttgtctaagatg 1644
 DB 1691 cagttgtctaagatg 1704

RESUFT 11

AAV23595
 ID AAV23595 standard: cDNA to mRNA; 1704 BP.
 AC AAV23595;
 XX 16-JUL-1998 (first entry)
 DE Antibody-Firefly Luciferase fusion protein gene.
 XX Firefly Luciferase; antibody-Luciferase fusion protein; ds.
 XX Luciola cruciata.
 OS
 XX
 XX
 XX
 FT Key Location/Qualifiers
 CDS 1..1704

FT /*tag= a
 FT /note= "no stop codon given"
 PN JP09187281-A.
 XX 22-JUL-1997.
 PD
 XX 09-JAN-1996; 96JP-0001812.
 PF
 XX 09-JAN-1996; 96JP-0001812.
 PR
 XX
 PA (KIKK) KIKKOMAN CORP.
 XX WPI: 1998-275089/25.
 DR P-PsDB; AAM53883.
 PT Antibody-firefly Luciferase fused protein - and related products
 PT i.e. firefly Luciferase fused gene, recombinant DNA and its
 PT preparation
 PS Disclosure; Page 10-11; 17pp; Japanese.
 CC This sequence encodes a fusion protein of the invention. The protein is
 CC a antibody-firefly Luciferase fusion protein, in which an antibody part
 CC consisting of a peptide having antibody activity is combined with an
 CC enzyme part consisting of firefly Luciferase.
 XX
 XX Sequence 1704 BP; 541 A; 275 C; 361 G; 527 T; 0 other:
 SQ
 Query Match 98.7%; Score 1622.8; DB 19; Length 1704;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1627; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 11 tggagaacgatgaataatgtgtatgtgtcctgaacattctccattgaagaagatg 70
 DB 71 tggagaacgatgaataatgtgtatgtgtcctgaacattctccattgaagaagatg 130
 QY 71 ctgtctgagacaaatgtgcgaagatatagtatgcatactgcaaaacttggaagatgct 130
 DB 131 ctgtctgagacaaatgtgcgaagatatagtatgcatactgcaaaacttggaagatgct 190
 QY 131 ttactaacgacttacccggtgtcgtatatacgtacgcggaatacttagaanaatcagct 190
 DB 191 ttactaacgacttacccggtgtcgtatatacgtacgcggaatacttagaanaatcagct 250
 QY 191 gtctagagaagagctttaaagaatatagtgtgtgtgtgtgtgaagaagatgtgtatga 250
 DB 251 gtctagagaagagctttaaagaatatagtgtgtgtgtgtgtgaagaagatgtgtatga 310
 QY 251 gtgaacacttgaagaattccttaattcctgattagcgggttatattatagtgctgctg 310
 DB 311 gtgaacacttgaagaattccttaattcctgattagcgggttatattatagtgctgctg 370
 QY 311 tggctccaactaatgagatttacactctacgtgattgtgtccaggtttagacatctcta 370
 DB 371 tggctccaactaatgagatttacactctacgtgattgtgtccaggtttagacatctcta 430
 QY 371 agccaacaattgtattagttcttaaaaaagattagaataagttatracgttcaaaaaa 430
 DB 431 agccaacaattgtattagttcttaaaaaagattagaataagttatracgttcaaaaaa 490
 QY 431 cgtgaactgtctataaacaactgttatatgacgaagaagtgatataagtgatc 490
 DB 491 cgtgaactgtctataaacaactgttatatgacgaagaagtgatataagtgatc 550
 QY 491 aatccatggaacacttattataaaaaaacctccacaaggttccaagaagtaagtttta 550
 DB 551 aatccatggaacacttattataaaaaaacctccacaaggttccaagaagtaagtttta 610
 QY 551 aaactgtagaagttaaacgcaaaagaagaagtgtgtcttataagaactctgggttcaa 610
 DB 611 aaactgtagaagttaaacgcaaaagaagaagtgtgtcttataagaactctgggttcaa 670

AAV23580	standard; CDNA to mRNA: 2364 BP.
AAV23580;	
16-JUL-1998	(first entry)
Antibody-Firefly Luciferase fusion protein gene.	
Firefly Luciferase; antibody-Luciferase fusion protein; ds.	
Luciola cruciata.	
Key	Location/Qualifiers
CDS	1..2364
	/*tag= a
	/transl_except= (pos: 670..672, aa: Glu)
	/transl_except= (pos: 739..741, aa: Trp)
	/transl_except= (pos: 1369..1371, aa: Ala)
	/note= "no stop codon given"
JP09187281-A.	
22-JUL-1997.	
09-JAN-1996;	96JP-0001812.
09-JAN-1996;	96JP-0001812.
(KIKK) KIKKOMAN CORP.	
WPI: 1998-275089/25.	
P-PSDB: AAW53882.	
Antibody-firefly Luciferase fused protein - and related products	
1.e. firefly Luciferase fused gene, recombinant DNA and its	
preparation	
Disclosure: Page 13; 17pp; Japanese.	
This sequence encodes the fusion protein of the invention. The protein is	
a antibody-firefly Luciferase fusion protein, in which an antibody part	
consisting of a peptide having antibody activity is combined with an	
enzyme part consisting of firefly Luciferase.	
Sequence 2364 BP: 697 A; 444 C; 559 G; 664 T; 0 other;	
Query Match	98.6%; Score 1621.6; DB 19; Length 2364;
Best Local Similarity	99.4%; Pred. No. 0;
Matches 1627; Conservative	0; Mismatches 9; Indels 0; Gaps 0;
9 catgagagaacatgaaatatgtgtgtaagtcctgtaaccatttaccctatgaaagag	68
729 cctcgagagacatgaaatatgtgtgtaagtcctgtaaccatttaccctatgaaagag	788
69 atctgctgagacacaattgagcgaagtatagtatgcatagaacaaacttgagcaattgc	128
789 atctgctgagacacaattgagcgaagtatagtatgcatagaacaaacttgagcaattgc	848
129 ttcttaccagcacttaccggtgctgcgattatagcagcgcgaactttagaanaaatcatg	188
849 ttcttaccagcacttaccggtgctgcgattatagcagcgcgaactttagaanaaatcatg	908
189 ctgtctagagagagcctttaaagaattatglttggtgttgtaatggaagaattgcgtatg	248
909 ctgtctagagagagcctttaaagaattatglttggtgttgtaatggaagaattgcgtatg	968
249 cagtgagaaactgctgaagaattccttatctcgtatttagcgggttatttattagtggtgcg	308
969 cagtgagaaactgctgaagaattccttatctcgtatttagcgggttatttattagtggtgcg	1028

QY 309 tttgtgtcccaataatgagatttaacactctacgtgaattgtgttcaacagtttaagcatctc 368
 Db 1029 tttgtgtcccaataatgagatttaacactctacgtgaattgtgttcaacagtttaagcatctc 1088
 QY 369 taaagcaacaattgtattttagttcttaaaaaagagattagataaatttaactgttacaana 428
 Db 1089 taaagcaacaattgtattttagttcttaaaaaagagattagataaatttaactgttacaana 1148
 QY 429 aacggtaactgtatlaaaacacattgttataatggacagaaagtgtatlaagagttta 488
 Db 1149 aacggtaactgtatlaaaacacattgttataatggacagaaagtgtatlaagagttta 1208
 QY 489 tcaatccatggacaactttatataaaacacatccacaaagtttcaagagtaaatgtt 548
 Db 1209 tcaatccatggacaactttatataaaacacatccacaaagtttcaagagtaaatgtt 1268
 QY 549 taaactgtagaagttaacccgaaagaagttgtcttataatgaactcttcgggttc 608
 Db 1269 taaactgtagaagttaacccgaaagaagttgtcttataatgaactcttcgggttc 1328
 QY 609 aacgggttgcacaaagggtgtgcaacttactcaatgaataattgttcaactagatttccca 668
 Db 1329 aacgggttgcacaaagggtgtgcaacttactcaatgaataattgttcaactagatttccca 1388
 QY 669 cgttagagatccaatttttgaaaccaagtttaccagagcaggtattttaaactgtagt 728
 Db 1389 cgttagagatccaatttttgaaaccaagtttaccagagcaggtattttaaactgtagt 1448
 QY 729 accattccatcatgtgttctgtatgttactactttagcttactcaacttctgtgttcg 788
 Db 1449 accattccatcatgtgttctgtatgttactactttagcttactcaacttctgtgttcg 1508
 QY 789 tattgtcatgtttaaagaaatttgacgaagagactttttaaaaaactgcgaagtataaa 848
 Db 1509 tattgtcatgtttaaagaaatttgacgaagagactttttaaaaaactgcgaagtataaa 1568
 QY 849 atgttcaacgcttattctctgtacgacttgttgaacttctttaaagaagttaatt 908
 Db 1569 atgttcaacgcttattctctgtacgacttgttgaacttctttaaagaagttaatt 1628
 QY 909 cgataataatgaattatcaaatlttagtgaattgacatctgcggagacacttactaa 968
 Db 1629 cgataataatgaattatcaaatlttagtgaattgacatctgcggagacacttactaa 1688
 QY 969 agaaattgttgaagctgtgtctagaagctttaaattaccgggtgtgtcgaaggtatag 1028
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 QY 1029 ttttaacagaacaacactctgcgaattatatacaccgggaagcgatgaataaccaggtgc 1088
 Db 1749 ttttaacagaacaacactctgcgaattatatacaccgggaagcgatgaataaccaggtgc 1808
 QY 1089 ttctggcaaaagtgtgccaattttaaagcaaaagttatcgatcttgaatactaaanaac 1148
 Db 1809 ttctggcaaaagtgtgccaattttaaagcaaaagttatcgatcttgaatactaaanaac 1868
 QY 1149 ttgtggcccgaaacagcgtggaaggtttgtttaaaggttctatagcttataaagttta 1208
 Db 1869 ttgtggcccgaaacagcgtggaaggtttgtttaaaggttctatagcttataaagttta 1928
 QY 1209 tttgaagtaatccagaagcaacaagaagaaatcatalagaagaaggttggttcacacag 1268
 Db 1929 tttgaagtaatccagaagcaacaagaagaaatcatalagaagaaggttggttcacacag 1988
 QY 1269 agatattgtgtattacgatgaagaanaaacattcttactcgttgatcgtttgaagcttt 1328
 Db 1989 agatattgtgtattacgatgaagaanaaacattcttactcgttgatcgtttgaagcttt 2048
 QY 1329 aatcaatacaagaagatcaagtaaccactgtgaataatgaataatcgttcttgcaca 1388
 Db 2049 aatcaatacaagaagatcaagtaaccactgtgaataatgaataatcgttcttgcaca 2108

QY 1389 tccaatatttttgatgcggcgttctgtgcgttccagatccatagatcgtgtgagcttcc 1448
 Db 2109 tccaatattttttgatgcggcgttctgtgcgttccagatccatagatcgtgtgagcttcc 2168
 QY 1449 gggagcgttctgtgttacttaagaagaatactatagactgaaagaagaatagatgata 1508
 Db 2169 gggagcgttctgtgttacttaagaagaatactatagactgaaagaagaatagatgata 2228
 QY 1509 cgttgcgtgacgaatttcaaatgcaaaagcttgcgtgtgtgtgtcgttctgtgagca 1568
 Db 2229 cgttgcgtgacgaatttcaaatgcaaaagcttgcgtgtgtgtgtcgttctgtgagca 2288
 QY 1569 agtacctaaggtctcactgtgtaaaattgacggtaaaagcaattagaagaatactagaaga 1628
 Db 2289 agtacctaaggtctcactgtgtaaaattgacggtaaaagcaattagaagaatactagaaga 2348
 QY 1629 accagttgctaagatg 1644
 Db 2349 accagttgctaagatg 2364

RESULT 13

AXX25717
 ID AAX25717 standard; cDNA to mRNA, 1656 BP.

XX AAX25717;

XX 21-MAY-1999 (first entry)

DE Firefly luciferase gene #3.

XX Bioluminescent protein: catalytic efficiency; stability; firefly;

KW luciferase; chimeric; luciola cruciata; luciola lateralis;

KW photinus pyralis; primer; PCR; amplification; ss.

OS Chimeric - Luciola lateralis.

XX Chimeric - Photinus pyralis.

XX W09902697-A1.

XX 21-JAN-1999.

XX 30-JUN-1998; 98W0-JP02936.

XX 08-JUL-1997; 97US-0051917.

XX (KIKK) KIKKOMAN CORP.

XX Hiokawa K, Kajiyama N, Murakami S;

XX WPI: 1999-120898/10.

XX P-PSDB: AAW93366.

XX New bioluminescent protein with improved properties - has greater

XX catalytic efficiency and stability and is obtained by modification

XX of natural precursors

XX Example 3; Page 30-31; 53pp; Japanese.

XX The invention relates to the generation of bioluminescent proteins with

XX improved catalytic efficiency and stability. The proteins are generated

XX by addition, deletion or substitution of amino acids from a precursor

XX protein e.g. firefly luciferases, or by constructing chimeric luciferase

XX proteins from luciferase genes from e.g. luciola cruciata, L. lateralis

XX and photinus pyralis. This sequence represents an example of a chimeric

XX luciferase gene of the invention.

Sequence 1656 BP; 529 A; 283 C; 366 G; 478 T; 0 other;

Query Match 90.9%; Score 1493.6; DB 20; Length 1656;

Best Local Similarity 94.8%; Pred. No. 0; Mismatches 84; Indels 0; Gaps 0;

Matches 1544; Conservative 0;

QY 1 atggaacaatggagaacga tgaatatgtatgtctgaaccatttaccatt 60
|||||
Db 1 atggaacaatggagaacga tgaatatgtatgtctgaaccatttaccatt 60
QY 61 gaagagagatcctgtagacacaat tgcgaagtata tgcgcgatatgcgaacttga 120
|||||
Db 61 gaagagagatcctgtagacacaat tgcgaagtata tgcgcgatatgcgaacttga 120
QY 121 gcaattgcttactaagcactacccggtgctgattatcctgaagcgcgaattacttagaa 180
|||||
Db 121 gcaattgcttactaagcactacccggtgctgattatcctgaagcgcgaattacttagaa 180
QY 181 aaatcgtctctaggaagagcgtttaaagaattatgtttgtttgttga tggagaatt 240
|||||
Db 181 aaatcgtctctaggaagagcgtttaaagaattatgtttgtttgttga tggagaatt 240
QY 241 gcgttatgcgtgtaaaactgttgaagaattccttaccgttataggcgggttattata 300
|||||
Db 241 gcgttatgcgtgtaaaactgttgaagaattccttaccgttataggcgggttattata 300
QY 301 ggtgtcgtgtgtgctccaactaattgaattactaactgaattgaattggttccagttta 360
|||||
Db 301 ggtgtcgtgtgtgctccaactaattgaattactaactgaattgaattggttccagttta 360
QY 361 ggcactcttaagccacaactatgtattagtcttaaaaaagagattagataaagtataact 420
|||||
Db 361 ggcactcttaagccacaactatgtattagtcttaaaaaagagattagataaagtataact 420
QY 421 gtacaaaaaagcgttaactcgttatataaaacattgttatatttgaacgaagaatgtgattat 480
|||||
Db 421 gtacaaaaaagcgttaactcgttatataaaacattgttatatttgaacgaagaatgtgattat 480
QY 481 agaggtatcaatccatctggaacacttatataaaaaaacctccacaaggtttcaagaaga 540
|||||
Db 481 agaggtatcaatccatctggaacacttatataaaaaaacctccacaaggtttcaagaaga 540
QY 541 tcaagttttaaaactgttagaagttaacgcgaagaacaaagltgctcttataatgaactct 600
|||||
Db 541 tcaagttttaaaactgttagaagttaacgcgaagaacaaagltgctcttataatgaactct 600
QY 601 tgggtgttcaacccggttgcgaagaaggtgtgcaactactcaatgaataattgtgcactaga 660
|||||
Db 601 tgggtgttcaacccggttgcgaagaaggtgtgcaactactcaatgaataattgtgcactaga 660
QY 661 ttctccacgctagagatccaaattttagaaccagaagttccaccagcagcgtatttta 720
|||||
Db 661 ttctccacgctagagatccaaattttagaaccagaagttccaccagcagcgtatttta 720
QY 721 actgtatgataccattccatcaatggtttgttgaatttactacttagcgtatcaactgtg 780
|||||
Db 721 actgtatgataccattccatcaatggtttgttgaatttactacttagcgtatcaactgtg 780
QY 781 ggtttcgtatgtcatgtttaacgaatttgaacgaagaactttttaaaacactgcaaa 840
|||||
Db 781 ggtttcgtatgtcatgtttaacgaatttgaacgaagaactttttaaaacactgcaaa 840
QY 841 gattacaatgttcaagcgttatctctgacgcgacttgttggcaatttcttaataagaagt 900
|||||
Db 841 gattacaatgttcaagcgttatctctgacgcgacttgttggcaatttcttaataagaagt 900
QY 901 gaattactcgaataatattatcaaatltagtgaattgcaatcgtcgtcgagaaact 960
|||||
Db 901 gaattactcgaataatattatcaaatltagtgaattgcaatcgtcgtcgagaaact 960
QY 961 ttacttaagaagaattgtgaagcgtgtgtcgaagcgttttaatttaacgggtgttcgtcaa 1020
|||||
Db 961 ttacttaagaagaattgtgaagcgtgtgtcgaagcgttttaatttaacgggtgttcgtcaa 1020
QY 1021 ggcatagtgttacaagaacacccctgcgaattattatataccacgggaagcgtatgataa 1080
|||||
Db 1021 ggcatagtgttacaagaacacccctgcgaattattatataccacgggaagcgtatgataa 1080

QY 1081 ccaagtgctctcggcaaaagtgtgccaattttaaagcaaaagttacatcttgatct 1140
|||||
Db 1081 ccaagtgctctcggcaaaagtgtgccaattttaaagcaaaagttacatcttgatct 1140
QY 1141 aaaaaaactttgggcccgcaacagacgttggagaagttgtgtlaaagggttcctatgtatg 1200
|||||
Db 1141 aaaaaaactttgggcccgcaacagacgttggagaagttgtgtlaaagggttcctatgtatg 1200
QY 1201 aaaggttatgtagaatccagaagcgaagaagaattcaatagatgaagaagttgtgt 1260
|||||
Db 1201 aaaggttatgtagaatccagaagcgaagaagaattcaatagatgaagaagttgtgt 1260
QY 1261 cacacagagatatgttggtatlaacgatgaagaacaaatttcttactcgtggaatcgtttg 1320
|||||
Db 1261 cacacagagatatgttggtatlaacgatgaagaacaaatttcttactcgtggaatcgtttg 1320
QY 1321 aagttcttaatcaatacaagaagatatacaagtlaccacacgtcgtgaattagaatcgttct 1380
|||||
Db 1321 aagttcttaatcaatacaagaagatatacaagtlaccacacgtcgtgaattagaatcgttct 1380
QY 1381 ttgcaatcccaaatattttttagtcggcggttgcgttccagatccatagctggt 1440
|||||
Db 1381 ttgcaatcccaaatattttttagtcggcggttgcgttccagatccatagctggt 1440
QY 1441 gaactccgggaagcgtgtgtgttacttaagaagaagaacatctactgaactgaagaagata 1500
|||||
Db 1441 gaactccgggaagcgtgtgtgttacttaagaagaagaacatctactgaactgaagaagata 1500
QY 1501 atgattatcgtgtcgtacgaagtttcaaatgcaaaacggttgcgtgtgtgtgtcgtttt 1560
|||||
Db 1501 atgattatcgtgtcgtacgaagtttcaaatgcaaaacggttgcgtgtgtgtgtcgtttt 1560
QY 1561 gtggacgaagttacttaaggtcactggttaaaattgacggttaagaagattagaagaata 1620
|||||
Db 1561 gtggacgaagttacttaaggtcactggttaaaattgacggttaagaagattagaagaata 1620
QY 1621 ctgaagaa 1628
|| |
Db 1621 ctcatataa 1628

RESULT 14
AAN91170
ID AAN91170 standard; DNA; 1644 BP.
XX
AC AAN91170;
DT 14-JUN-1990 (first entry)
XX
DE Recombinant luciferase gene.
XX
KW Luciferase; ATP assay; ss.
OS Luciola cruciata.
PN EP301541-A.
XX
PD 01-FEB-1989.
XX
PE 28-JUL-1988; 88EP-0112233.
XX
PR 29-JUL-1987; 87JP-0187724.
PR 29-JUL-1987; 87JP-0187725.
PR 20-AUG-1987; 87JP-0205194.
XX
PA (KIKK) KIKKOMAN CORP.
PI Masuda T, Tatsumi H, Nakano E;
XX
XX
DR MPI: 1989-033443/05.
XX
XX P-PSDB; AAP94367.
PT Recombinant luciferase gene - used for efficiently producing luciferase

in E. coli, obtaining a stable and highly active prod.
PS Claim 2; fig 3; 35pp; English.

The sequence was obtd. from cDNA prepd. from mRNA isolated from
CC L. cruciata tails. The DNA can be incorporated into vectors for
CC transformation of E. coli JM 1010.

Sequence 1644 BP; 529 A; 276 C; 338 G; 501 T; 0 other;

Query Match 82.5%; Score 1356; DB 10; Length 1644;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 1 atcgaaacatgagagacatgaaatattgtatgctgcctgaaccatttaccatt 60
DB 1 atcgaaacatgagagacatgaaatattgtatgctgcctgaaccatttaccatt 60
QY 61 gaaagaggatctgtcgtgagacacatgctgcaaglatatgatgcataatctgga 120
DB 61 gaaagaggatctgtcgtgagacacatgctgcaaglatatgatgcataatctgga 120
QY 121 ggaattgctttactaacgcacttaccggtgtcogattatacgtacgcgaattagaa 180
DB 121 ggaattgctttactaacgcacttaccggtgtcogattatacgtacgcgaattagaa 180
QY 181 aaatcatgctgtcgtgagagagctttaagaattatggtttgtttatgagaatt 240
DB 181 aaatcatgctgtcgtgagagagctttaagaattatggtttgtttatgagaatt 240
QY 241 gcgttatgcagtgaanaactgtgaagaattcttattcctgataagcggttattata 300
DB 241 gcgttatgcagtgaanaactgtgaagaattcttattcctgataagcggttattata 300
QY 301 ggttcggtgtgtgcccactaaatgagattacactctcgtgaattgtgttcaagttta 360
DB 301 ggttcggtgtgtgcccactaaatgagattacactctcgtgaattgtgttcaagttta 360
QY 361 ggcattctctaaagcaacaattgtatttatttcttaaaaaagattatagaattaaact 420
DB 361 ggcattctctaaagcaacaattgtatttatttcttaaaaaagattatagaattaaact 420
QY 421 gtaacaaaaacggtatcgtctatataaacacattgtatatactgacagcaaatgtat 480
DB 421 gtaacaaaaacggtatcgtctatataaacacattgtatatactgacagcaaatgtat 480
QY 481 aaggttatcaatccatgacacatttatataaaaaaacaccccaagtttcaagaa 540
DB 481 aaggttatcaatccatgacacatttatataaaaaaacaccccaagtttcaagaa 540
QY 541 tcaagttttaaactgtgaagttaaccgcaagaacaagttgtctctttaaataactct 600
DB 541 tcaagttttaaactgtgaagttaaccgcaagaacaagttgtctctttaaataactct 600
QY 601 tccagtttcaaaaacgttgaaagttagcgttaagaacaagttgtctctttaaataactct 660
DB 601 tccagtttcaaaaacgttgaaagttagcgttaagaacaagttgtctctttaaataactct 660
QY 661 tttctcagctagagatcccaatttatatgaaaacaaagtttcaacggcagctattta 720
DB 661 tttctcagctagagatcccaatttatatgaaaacaaagtttcaacggcagctattta 720
QY 721 actgtagtaccatccatcatggtttgtgatacttactactgtgcatcactatgt 780
DB 721 actgtagtaccatccatcatggtttgtgatacttactactgtgcatcactatgt 780
QY 781 ggttcgtatgtcatgttaacgaatttgaacgaagaaactttttaaacaactgcga 840
DB 781 ggttcgtatgtcatgttaacgaatttgaacgaagaaactttttaaacaactgcga 840
QY 841 gattcaaatgttcaagcgttatcttctgacgcacttgttgcgaatttcttaagaatt 900
DB 841 gattcaaatgttcaagcgttatcttctgacgcacttgttgcgaatttcttaagaatt 900

DB 841 gattcaaatgttcaagcgttatcttctgacgcacttgttgcgaatttcttaagaatt 900
QY 901 gaattctcgataataatgatttatacaaatattgttgaatttgcatttgcggagaccc 960
DB 901 gaattctcgataataatgatttatacaaatattgttgaatttgcatttgcggagaccc 960
QY 961 ttactcaagaanaattgttgagcgtgtgtcagacgtttaaatttaccgggtgtcgtcaa 1020
DB 961 ttactcaagaanaattgttgagcgtgtgtcagacgtttaaatttaccgggtgtcgtcaa 1020
QY 1021 ggcatagttttaacagaacaacctctgcataattatcaacaccggaagcgatgataa 1080
DB 1021 ggcatagttttaacagaacaacctctgcataattatcaacaccggaagcgatgataa 1080
QY 1081 cccaggtgtcttcgtgcaaaagtgtgcattatattaaagcaaaacttaccgttctgact 1140
DB 1081 cccaggtgtcttcgtgcaaaagtgtgcattatattaaagcaaaacttaccgttctgact 1140
QY 1141 aaaaaaacttggccgcaacagctggaagaagttgtgttaaaaggtccatgctatg 1200
DB 1141 aaaaaaacttggccgcaacagctggaagaagttgtgtgttaaaaggtccatgctatg 1200
QY 1201 aaagttatgtatataatccagaagaacaagaagaatcatagatgaagaagttggtg 1260
DB 1201 aaagttatgtatataatccagaagaacaagaagaatcatagatgaagaagttggtg 1260
QY 1261 cacacaggagatattgtttagatccgatgaaagaacattcttaccgtgagatctgtg 1320
DB 1261 cacacaggagatattgtttagatccgatgaaagaacattcttaccgtgagatctgtg 1320
QY 1321 aagctttaaatacaatacaagaagatatacaagtaacacctctgtaattagatctgtct 1380
DB 1321 aagctttaaatacaatacaagaagatatacaagtaacacctctgtaattagatctgtct 1380
QY 1381 ttgcaacatcccaatatttttgaatccgcggtgtgtgtgtccagatccataagctgtg 1440
DB 1381 ttgcaacatcccaatatttttgaatccgcggtgtgtgtgtgtccagatccataagctgtg 1440
QY 1441 gagcttcgggagcgtgtgtgttacttaagaagaagaatactatgactgaaagaagta 1500
DB 1441 gagcttcgggagcgtgtgtgttacttaagaagaagaatactatgactgaaagaagta 1500
QY 1501 atggtatcgtgtgcaagtcgaagtttcaaatgtaaaagtttgaagttggtgtgtt 1560
DB 1501 atggtatcgtgtgcaagtcgaagtttcaaatgtaaaagtttgaagttggtgtgtt 1560
QY 1561 gtgagcgaagctactaaagttccactgtgtataatgtgacgtgtaagaatgaagaata 1620
DB 1561 gtgagcgaagctactaaagttccactgtgtataatgtgacgtgtaagaatgaagaata 1620
QY 1621 ctgaagaacaacgttctgaagatg 1644
DB 1621 ctgaagaacaacgttctgaagatg 1644

RESULT 15
AA003801
ID AA003801 standard; cDNA; 1644 BP.
XX
AC AA003801;
XX
DT 22-AUG-1990 (first entry)
XX
DT 26-FEB-1993 (revised entry)
XX
DE Recombinant luciferase gene.
XX
KW Luciferase; ATP; E. coli; photon; ds.
XX
OS Synthetic.
XX
PN JP02065780-A.
XX
PD 06-MAR-1990.

XX 01-SEP-1988: 88JP-0216229.
XX 01-SEP-1988: 88JP-0216229.
XX (KIKK) KIRKMAN CORP.
XX WPI: 1990-113360/15.
XX P-PSDB: AAR05788.
DR Prepn. of luciferase -
XX using Escherichia sp. bacteria contg. recombinant DNA.
XX
XX Prepn. of luciferase -
XX using Escherichia sp. bacteria contg. recombinant DNA.
XX
XX Claim 2: Page 416 + Fig 3; 20pp; Japanese.
XX
XX Prepn. of luciferase comprises culturing Escherichia sp. contg.
XX recombinant DNA, and harvesting luciferase from the culture medium.
XX The recombinant DNA is a vector DNA into which has been inserted the
XX luciferase gene which has the nucleotide sequence below. Luciferase
XX can be produced quickly and efficiently with an increased photon
XX output, useful in assaying ATP.
XX
XX Sequence 1644 BP; 529 A; 276 C; 338 G; 501 T; 0 other;

Query Match 82.5%; Score 1356; DB 11; Length 1644;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 1 atggaacaatggaagaatgaataatgtagtgcctgaaccatttaccctat 60
DB 1 atggaacaatggaagaatgaataatgtagtgcctgaaccatttaccctat 60
QY 61 gaagagagatctctgagacacatttgcgaagtatagatcgatatgcaaaacttga 120
DB 61 gaagagagatctctgagacacatttgcgaagtatagatcgatatgcaaaacttga 120
QY 121 gcaattccttactaaccgactacacgtgctgcattatcgtaacgcgcgaatacttga 180
DB 121 gcaattccttactaaccgactacacgtgctgcattatcgtaacgcgcgaatacttga 180
QY 181 aatcatgctctgtagagagagccttaagaatatagtgtgttgcgtgagagaat 240
DB 181 aatcatgctctgtagagagagccttaagaatatagtgtgttgcgtgagagaat 240
QY 241 ggcattagcagtgaaacttgaagaattcttattcctgtattagccggtttata 300
DB 241 ggcattagcagtgaaacttgaagaattcttattcctgtattagccggtttata 300
QY 301 ggtgtaggtgttgacacacattgaattacacattgaagtcggttcaagttta 360
DB 301 ggtgtaggtgttgacacacattgaattacacattgaagtcggttcaagttta 360
QY 361 ggcattcctaagcacaatttatttatttcttaaaaaagattagataaagtataact 420
DB 361 ggcattcctaagcacaatttatttatttcttaaaaaagattagataaagtataact 420
QY 421 gtcaaaaaacgtagtactgtatttaaaacattgttatattgacacaaagtgtat 480
DB 421 gtcaaaaaacgtagtactgtatttaaaacattgttatattgacacaaagtgtat 480
QY 481 agaggtatcaatcagcgaacttatttaaaaaaacactccacaaagtttcaagga 540
DB 481 agaggtatcaatcagcgaacttatttaaaaaaacactccacaaagtttcaagga 540
QY 541 tcaagtttaaaactgtagaagttaaccgaaagaacaaagttgcttataatgaact 600
DB 541 tcaagtttaaaactgtagaagttaaccgaaagaacaaagttgcttataatgaact 600
QY 601 tcgggttcaacccggttgcaaaaagtgctgaacttactatgaaatttggtcactaga 660
DB 601 tcgggttcaacccggttgcaaaaagtgctgaacttactatgaaatttggtcactaga 660

QY 661 ttctcaccgtagagatcccaatttattgaaacccaagtttccaccgagcgtatttta 720
DB 661 ttctcaccgtagagatcccaatttattgaaacccaagtttccaccgagcgtatttta 720
QY 721 actgtagtaccatccatcattggttggtagtcttactacttaggtactaactgt 780
DB 721 actgtagtaccatccatcattggttggtagtcttactacttaggtactaactgt 780
QY 781 gttttgtagtgcagtagtgaagaatttgaagaagaagctttttaaacaactgca 840
DB 781 gttttgtagtgcagtagtgaagaatttgaagaagaagctttttaaacaactgca 840
QY 841 gattacaatgccaagcatttctgtacacagcttgttgcacattcttaataagaat 900
DB 841 gattacaatgccaagcatttctgtacacagcttgttgcacattcttaataagaat 900
QY 901 gaattactgataaattatgattatcaaatattgattgaattgcatctgcgagacact 960
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QY 961 ttacttaagaagaattgtagaagcgtgtgctgtagaagcttattaccgggtgttcga 1020
DB 961 ttacttaagaagaattgtagaagcgtgtgctgtagaagcttattaccgggtgttcga 1020
QY 1021 ggcattggtttaaacaagaacacactctgcaattatataccaccggaagcgatgataa 1080
DB 1021 ggcattggtttaaacaagaacacactctgcaattatataccaccggaagcgatgataa 1080
QY 1081 ccaggtgctctcgcgcaagctgtgctgctatataagaacaaagttatcgatctgatact 1140
DB 1081 ccaggtgctctcgcgcaagctgtgctgctatataagaacaaagttatcgatctgatact 1140
QY 1141 aaaaaaactctgagcgaagaagcgtgaggaagttgtgtaagaaagttatctgatacc 1200
DB 1141 aaaaaaactctgagcgaagaagcgtgaggaagttgtgtaagaaagttatctgatacc 1200
QY 1201 aaagttatgtagataatccagaagaacaaagaaatcatalagataagaagttgtgtg 1260
DB 1201 aaagttatgtagataatccagaagaacaaagaaatcatalagataagaagttgtgtg 1260
QY 1261 caccagagagatatgtgtattacgtagaagaagaacatttcttaccggtgactgtt 1320
DB 1261 caccagagagatatgtgtattacgtagaagaagaacatttcttaccggtgactgtt 1320
QY 1321 aagctttaaatacaatacaagaagatcaagtaaccactgcggaattagaatccgttct 1380
DB 1321 aagctttaaatacaatacaagaagatcaagtaaccactgcggaattagaatccgttct 1380
QY 1381 ttgcaacatccaaatattttgtagtgcggtgtgctggtccagatccctataactgtgt 1440
DB 1381 ttgcaacatccaaatattttgtagtgcggtgtgctggtccagatccctataactgtgt 1440
QY 1441 gagcttcggagagcgtgtgtgtgtacttaagaagaagaacatctagactgaaagaagta 1500
DB 1441 gagcttcggagagcgtgtgtgtgtacttaagaagaagaacatctagactgaaagaagta 1500
QY 1501 atggtattcgtttagtgaagttcaaatgcaaatgcaaatgcaaatgcaaatgcaaatg 1560
DB 1501 atggtattcgtttagtgaagttcaaatgcaaatgcaaatgcaaatgcaaatgcaaatg 1560
QY 1561 gtgagcgaagtagcctaagaagtcactgtgtaaaattgaacggttaagaagaata 1620
DB 1561 gtgagcgaagtagcctaagaagtcactgtgtaaaattgaacggttaagaagaata 1620
QY 1621 ctgagaagaacccagttgtagatg 1644
DB 1621 ctgagaagaacccagttgtagatg 1644

Search completed: September 6, 2002, 19:38:41
Job time: 10'69 sec

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•

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 15:17:17 ; Search time 113.65 Seconds
(without alignments)
3553.203 Million cell updates/sec

Title: US-09-581-241-3
Perfect score: 1644
Sequence: 1 atggaacacatgagacga.....agaacacagtgtaagatg 1644

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/1na/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/1na/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/1na/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/1na/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/1na/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	1639.2	99.7	1644	US-09-111-752-13	Sequence 13, Appl
2	1636	99.5	1644	US-07-903-047-7	Sequence 7, Appl
3	1636	99.5	1644	US-09-380-061B-15	Sequence 15, Appl
4	1631.4	99.2	1908	US-08-460-934-8	Sequence 8, Appl
5	1631.4	99.2	1908	US-08-782-118-8	Sequence 8, Appl
6	1622.8	98.7	1704	US-08-460-934-5	Sequence 5, Appl
7	1622.8	98.7	1704	US-08-782-118-5	Sequence 5, Appl
8	1356	82.5	1644	US-07-675-211-1	Sequence 1, Appl
9	1356	82.5	1644	US-07-903-047-1	Sequence 1, Appl
10	1356	82.5	1644	US-08-076-042-1	Sequence 1, Appl
11	1356	82.5	1644	US-08-757-046A-3	Sequence 3, Appl
12	1356	82.5	1644	US-09-447-308-3	Sequence 3, Appl
13	1356	82.5	1644	US-09-135-988-3	Sequence 3, Appl
14	1356	82.5	1644	US-09-277-116-3	Sequence 3, Appl
15	1356	82.5	1644	US-08-597-274A-3	Sequence 3, Appl
16	1356	82.5	1644	US-09-380-061B-13	Sequence 13, Appl
17	1263.2	76.8	1656	US-09-111-752-8	Sequence 8, Appl
18	1040.8	63.3	1656	US-09-111-752-6	Sequence 6, Appl
19	1040.8	63.3	1656	US-09-111-752-9	Sequence 9, Appl
20	1014.4	61.7	2009	US-09-380-061B-17	Sequence 17, Appl
21	818.8	49.8	1725	US-09-380-061B-19	Sequence 19, Appl
22	745.8	45.4	5427	US-09-282-996-2	Sequence 2, Appl
23	745.2	45.3	1811	US-08-867-352-22	Sequence 22, Appl
24	745.2	45.3	1811	US-08-867-352-22	Sequence 32, Appl
25	745.2	45.3	5791	US-08-862-431-31	Sequence 31, Appl
26	745.2	45.3	5793	US-08-862-431-29	Sequence 29, Appl
27	745.2	45.3	5793	US-08-862-431-30	Sequence 30, Appl

28	745.2	45.3	5818	US-08-536-559A-3	Sequence 3, Appl
29	745.2	45.3	5819	US-08-536-559A-2	Sequence 2, Appl
30	745.2	45.3	5819	US-08-862-431-27	Sequence 27, Appl
31	745.2	45.3	5819	US-08-862-431-28	Sequence 28, Appl
32	745.2	45.3	5938	US-08-536-559A-4	Sequence 4, Appl
33	745.2	45.3	6092	US-08-536-559A-1	Sequence 1, Appl
34	745.2	45.3	6092	US-08-862-431-26	Sequence 26, Appl
35	745.2	45.3	11616	US-08-196-259-2	Sequence 2, Appl
36	744	45.3	1722	US-09-380-061B-1	Sequence 1, Appl
37	743.6	45.2	1650	US-08-354-240A-1	Sequence 1, Appl
38	743.6	45.2	2445	US-08-122-520C-8	Sequence 8, Appl
39	743.6	45.2	5620	US-08-793-170-21	Sequence 21, Appl
40	743.6	45.2	5620	US-08-892-873-21	Sequence 21, Appl
41	743.6	45.2	5620	US-09-334-765A-21	Sequence 21, Appl
42	743.6	45.2	5620	US-09-356-575E-21	Sequence 21, Appl
43	743.6	45.2	5620	US-09-333-820-21	Sequence 21, Appl
44	743.6	45.2	6044	US-08-316-950-18	Sequence 18, Appl
45	743.6	45.2	6044	PCT-US95-12642-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-111-752-13
; Sequence 13, Application US/09111752
; Patent No. 6074859
; GENERAL INFORMATION:
; APPLICANT: HIROKAWA, KOZO
; APPLICANT: KATAYAMA, NAOKI
; APPLICANT: MURAKAMI, SEIJI
; TITLE OF INVENTION: MUTANT-TYPE BIOLUMINESCENT PROTEIN, AND
; TITLE OF INVENTION: PROCESS FOR PRODUCING MUTANT-TYPE BIOLUMINESCENT PROTEIN
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,752
; FILING DATE: 08-JUL-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 7126-0009-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1644 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORGANISM: Luciola lateralis
; US-09-111-752-13
Query Match 99.7%; Score 1639.2; DB 3; Length 1644;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1641; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 atggaacatgagagacatgaaatattgtgtatgtgtccctgaaccatttaccctatt 60
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Db 1 ATGGAAAAATGAGAGAACATGAAAAATTGTTGTTATGTCCTGACCATTTTAACTCCCTATT 60
OY 61 gaagaaaggaatctgtgagacacaaatgtgcgaagtataatgatcgtatatacgaactgtga 120
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Db 61 GAAGAGGAGATCTGCTGAGACACAAATTGGCAAGTATATGATGATGATGCAAAACTTGGG 120
OY 121 gcaatgtcttactaaccgacttaccggtgtcgtatatacgtacgcccgaattcttga 180
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Db 121 GCAATTTGCTTTTACTAACCCACTTACCGGTGTCGATTATACGTACCCCGAATCTTAGAA 180
OY 181 aatactgtctcgaagagagcctttaaagaattatgattgtgtgtgtgtatgaagaatt 240
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Db 181 AATCATGCTGCTCTAGAGAGGCTTTAAAGAAATATGCTTTGTTGTTGATGGAAGAAATT 240
OY 241 gcgctatgcaatgaaactgtgaagaattcttattcctglatagccggtttattata 300
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Db 241 GCGTATGCAAGTGAAGAACTGTGAAGAAATTCTTATTCCTGATTATAGCCGGTTATTTATA 300
OY 301 ggtgtcgtgtgtgtcctaataatgattatcactctcagatgtgtatgtgtcacttca 360
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Db 301 GGTGTGCGGTGTGCTCAACTAATGAGATTACACTCTACGTGAATTTGGTTCACAGTTTA 360
OY 361 ggcattcctcaagccaaactgttattatgttctcaaaaagatagataaagtataact 420
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Db 361 GGCATCTCAAGCCAAACATTTGATTAGTTCTCAAAAAAGATTAATATAAGTTATTAAC 420
OY 421 gtcaaaaaacggttaactgtctatlaaacaattgtatatatgtgacagcaagtgtactat 480
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Db 421 GTACAAAAAACGTTAACTCTATTAAACCATTTGTTATATTGACAGCAAGAGGATATTAT 480
OY 481 aagagttacaatccatgagacaacttattataaaaaaacactcacaagtttcaaga 540
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Db 481 AAGAGGTTATCAATCCATGAGACACTTTATTAATAAAAAACACTCCACAAGGTTTCAAGGA 540
OY 541 tcaagttttaaactgtlaagaagttaaccgcaagaacaggtgtctatataatgaactct 600
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Db 601 TCGGGTTCAACCGGTTTGGCAAAAGGTGTGCAACTTACTCATGAAATTTGGTGATCTG 660
OY 661 ttcttcacgcttagagataccaattatgaaaccaagtttccccaacggtatttca 720
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Db 661 TTTTCTCACGCTAGAGATCCAAATTATAGGAACCAAGTTTCACAGGACAGGCTATTTTA 720
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Db 721 ACTGTATGATCAATTCATCATGATGTTGGTATGTTACTACTTACGCTATCACTAATCTG 780
OY 781 ggttttcgtattgtcatgttaacgaaatttgacgaagagactttttaaacaactgtcaa 840
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Db 781 GGTTTTCGTATTGTCTATGTTAAAGAAATTTGAAGAGACTTTTAAAAACACTGCAA 840
OY 841 gattcaaaatgttcaaggtttatcttcttgaacgactttgttgaatttcaataagaat 900
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Db 841 GATTCAAAATGTCAAGCGTTATCTTGTGACGACTTTGTCGAATTTCTTAATTAAGAG 900
OY 901 gaattactcgaataatataatcatcaaatltagtgaattgcaactgtgcggaacact 960
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Db 901 GAATTACTCGATAAATATATATTATCAAAATTTAGTTGAATTCGACTGTGGGAGACACT 960
OY 961 ttactcaagaatgttggtagaagcgtgtgtctagaagcgtttaaattacgggtgtgtc 1020
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Db 961 TTATCTAAAGAAATTTGTTGAAGCTGTTGCTAGACGTTTAAATTTACCGGGTGTGCTCAA 1020
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Db 1021 GGCTATGTTTAAACAAACACTCTGCAATTATTATATCAACACCGGAAGCGATGATATA 1080

OY 1081 ccaggtcctctggcaaaagtgtgccaattttaaagcaaaagtatacgaattcgtatc 1140
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Db 1081 CCAGGTCTCTTCTGCAAAAGTGTGCCATTATTTAAAGCAAAAGTTATCGATCTTGATACT 1140
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Db 1141 AAAAAACTTTGGCCCGCAACAGCTGAGAGATTGTTGTTAAAGGTTCTTATGCTTATG 1200
OY 1201 aaggttataatataatccagaagaacaagaagaatcatatgaatgaagaagttgttg 1260
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Db 1201 AAGGTTATGTATATATCCAGAAACACAAAGAAATCATAGATGAAGAGGTTGCTTG 1260
OY 1261 cacacagagataatgtgatacgaatgaagaacaaacttcttactcgtgtgtcgtt 1320
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Db 1261 CACACAGAGATATTGGTATTTACGATGAAGAAACATTTCTTATTCGTGATTCGTTTG 1320
OY 1321 aagtttcaatcaatacaaaagataatcaagtaaccactgtcgaattagaattcgtctt 1380
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Db 1321 AAGTCTTTAATCAAAATACAAAGGATATCAAGTACCACTGTAATTAGAATCTGTTCTT 1380
OY 1381 ttgcaaatccaaatattttttagtcgaggtgtgtcgtgtccagatccctatagttgt 1440
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Db 1381 TTGCAAACTCCAAATATTTTGTATGCGGCGTGTGCTGCTCCAGATCTATAGCTGGT 1440
OY 1441 gaagttccgggaagctgtgtgtgtacttaagaagaagaactatactgaactgaaga 1500
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Db 1441 GAGCTTCCGGGAGACTGTGTGTGTACTTAAGAAAGAAATCTATGACTGAAAAAGATA 1500
OY 1501 atgattatcgttgtcgtatgaagtttcaaatgtcaaatgcgttgcgtgtgtgtcgtt 1560
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Db 1501 ATGATTACGTTCTGTGCTCAAGTTTCAAATGCAAAACGTTGGCTGTGCTGCTGCTGCT 1560
OY 1561 gtgacgaaggttacttaaggttctcactgtgtaaaattgacggttaagaatgaagaata 1620
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Db 1561 GTGACGAAGTACTTAAGGTTCTCACCTGTAATATTGACGCTAAAGCAATTTAGAGAAATA 1620
OY 1621 ctgaagaacacagttgtctaagatg 1644
|||||
Db 1621 CTGAAGAAACCACTGTCTAAGATG 1644

RESULT 2
US-07-903-047-7
; Sequence 7, Application US/07903047
; Patent No. 5229285
; GENERAL INFORMATION:
; APPLICANT: Kaiyama, Naoki
; APPLICANT: Nakano, Eichi
; TITLE OF INVENTION: Thermostable Luciferase Of Firefly,
; TITLE OF INVENTION: Thermostable Luciferase Gene Of Firefly, No. 5229285el Reco
; TITLE OF INVENTION: DNA, And Process For The Preparation Of Thermostable
; TITLE OF INVENTION: Luciferase Of Firefly
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/903,047
; FILING DATE: 19920623
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18, 872
; REFERENCE/DOCKET NUMBER: 7005-048

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090
TELEFAX: 212 869-8664/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1644 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: cDNA to mRNA

US-07-903-047-7

Query Match 99.5%; Score 1636; DB 1; Length 1644;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 atggaacacatggaacatgtaataatgtgtatgttcctgaacatttaccctatt 60
 DB 1 ATGGAACACATGGAACATGTAATAATGTGTATGTCTCTGAACCATTTTACCTATT 60
 QY 61 gaagaggaatctgtgagacaaatgagcaagatataatgataatgcaaaacttga 120
 DB 61 GAAGAGGAACTGTGAGACAAATGAGCAAGATATATGATGATATGCAAAACTTGA 120
 QY 121 gcaatgtcttactaaagcaactacgggtgtgattataatgtagccgaatttga 180
 DB 121 GCAATGTCTTACTAAAGCAACTACGGTGTGATTATAGCGCGCAATCTTGA 180
 QY 181 aaatcatgctgtcgaagagagcttaagaattatggttgtgttgaatgagaatt 240
 DB 181 AAATCATGCTGTGAGAGAGCTTAAAGAAATATGTTGTTGTTGATGAGAAAT 240
 QY 241 gcatatgacatgaaactgtgaagaattcttattccctgataagccggttata 300
 DB 241 GCGTATGACATGAAACTGTGAAGAAATCTTATCTCTGATTAGCGCGTTTATTATA 300
 QY 301 ggtgcggtgtggtgcacaaatgagaattacactgaagattggttcaagatt 360
 DB 301 GGTGCGGTGTGCTCCAACTAATGAGATTTACACTGACGTGAATGTTGACAGTTTA 360
 QY 361 ggcactcgaagcaacatgtatattgttctaaaaaagattagataaagttata 420
 DB 361 GGCATCTCTAGCCACACATTTGTTAGTTCTAAAAAAGATTAGATAAAGTTATACT 420
 QY 421 gtacaaaaacggttaactgtctataaaacatgltatattgagcaagagtgat 480
 DB 421 GTACAAAAACGGTAACTGCTATTAAAAACATTTGTTATTGACAGCAAGTGGATTAT 480
 QY 481 agaggtatcaatcactgacactttataaaaaaacatccaaagtttcaagga 540
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 DB 541 TCAAGTTTAAAACTGTGAAGTTTACCGCAAGAACAAGTTGCTTATATATGAACCT 600
 QY 601 tcgggttcaacgggttgcacaaagtggtcaacttactatgaaaatttgcact 660
 DB 601 TCGGTTCAACGGGTTTCCCAAAAGTGTGCAAACTTACTCATGAAATGCACTAC 660
 QY 661 ttttctacgctgaagatcccaattatggaacaaagtttcaacgaagcggtc 720
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 QY 781 ggttcgtatgtcattgtaagaatttgaagaagactttttaaacaactgca 840
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 DB 841 GATTACAAATGTTCAAGCGTATTCTGTACCGACTTGTTCGCAATTTCTAATGA 900
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 DB 1021 GGTATGTTTAAAGCAAAACACTCTGCATATTATATATACACCGGAAGCGAT 1080
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 DB 1081 CCAAGTGTCTTGTGCAAAAGTTGTCCATTATTAAAGCAAAAGTTATCGATCT 1140
 QY 1141 aaaaaaacttgggcccgaagacgtggaagattgtgtaaggttccatgctat 1200
 DB 1141 AAAAAAATTTGGGCCGCAAGACAGCGTGAAGTTGTGTAAGGTTCTATGCT 1200
 QY 1201 aaagttatgtaataatccagaagcaacagaagaataatagaagaagttgt 1260
 DB 1201 AAAGTTATGTAGTANTATCCAGAACACAGAAATCATATGATNAGAAGTTG 1260
 QY 1261 cacacagagataatggtatatacgaatgaagaacacatttcttactcgtg 1320
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 QY 1321 aagtttcaatcaatacaagaagataatcaagttccactcgtgtgaattga 1380
 DB 1321 AAGTTTAAATCAAAATCAAAAGATATCAAGTACCACTGCTGAATTAGAAT 1380
 QY 1381 ttgcaatccaaatatttctgtgcggtgtgtgcgttcgaatccatagctgt 1440
 DB 1381 TTGCAATCCAAATATTTTGTGATGCGCGCTGCTGCGCTTACATCTATAG 1440
 QY 1441 gagttccggagcgtgtgtgttacttaagaagaacatactgactgaagaaga 1500
 DB 1441 GAGTTCCGGAGCTGTTGTTGTTACTTGAAGAAAGAAATCTATGACTGAA 1500
 QY 1501 atggtatcgtgtgtgactgaagtttcaaatgcaaaagttgtgtgtgtgt 1560
 DB 1501 ATGATTTACGTTGCTAGTCAAAATTTCAAAAGCAAAAGTTGCTGTGCT 1560
 QY 1561 gtgagcgaagttactaaagttcactggtgaatgaatgaaggttaagaaga 1620
 DB 1561 GTGAGCAAGTACTTAAGGTTCTCAGTGTGTAATTTGACGTTAAGCAAT 1620
 QY 1621 ctgaagaacacgtgtgtaagatg 1644
 DB 1621 CTGAAGAACACAGTTGCTAAGATG 1644

RESULT 3

US-09-380-061B-15

; Sequence 15, Application US/09380061B

; Patent No. 6265177

; GENERAL INFORMATION:

; APPLICANT: SQUIRELL, DAVID JAMES

; WHITE, PETER JOHN

; LOWE, CHRISTOPHER ROBIN

; MURRAY, JAMES AUGUSTUS HENRY

; TITLE OF INVENTION: ENZYME ASSAY FOR MUTANT FIREFLY LUCIFERASE

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERBYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,061B
FILING DATE: 25-Apr-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01026
FILING DATE: 7-Apr-1998
APPLICATION NUMBER: GB 9707468.8
FILING DATE: 11-Apr-1997
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 124-725
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1644 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1644
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
us-09-380-061B-15

Query Match 99.5%; Score 1636; DB 4; Length 1644;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 atggaacaatggaagaatgaataatggtatgctcgaaccatttaccctatt 60
DB 1 ATGGAAACATGGAAGAACATGAAATATTGTATGTCCTGAACCATTTTACCTATT 60
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DB 61 GAAGAGGATCTGCTGAGACCAATTTGCCAAGTATATGATGATGCATAAATTTGA 120
QY 121 gcaattgcttacttaacacactaccggtgctgattacgtaacgcaactataga 180
DB 121 GCAATTGCTTTACTTAACGCACTTACCGGTGTCGATTATACGTACGCCAATTTAGTA 180
QY 181 aaatcatgctctcaggaagagctttaaagaattatggttggttgtaaggaagt 240
DB 181 AAATCATGCTCTCAGGAGAGGCTTTAAAGATTTATGTTGGTTGATGATGAAGAAAT 240
QY 241 ggcattacagtggaagaactgtaagaattcttattccgtgtaacggttattata 300
DB 241 GCGTTATGCAAGGAAACTGTGAAGAAATTTCTTTATTCCTGATTTAGCCGGTTATTTATA 300
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DB 301 GGTGTCGCTGGTGCCTCAACTATGAGATTTTACACTCTACGTAATGTTGTTACAGTTTA 360
QY 361 ggcattcttaagccaacaattgtatttagttctaaagaaagatagataaagtataact 420
DB 361 GGCATCTCTTAAGCCAAACATTTGTATTGATCTAAAGAAAGATTAAGTAAAGTTAACT 420
QY 421 gtacaaaacacgttaacgtctatttaaaccattgttatatggaagcaagtgattat 480
DB 421 GTACAAAACACGTTACTGCTATTATAAACCATTTGTTATTTGGAAGCAAAAGTGATTTAT 480

QY 481 ageggttacaatccatgagacaacttattaaaaaacaccacaaagtttcaaaga 540
DB 481 AGAGGTTATCAATCAATGAGCAACTTTATTAAAAAACCTCCACAGGTTTCAAGGA 540
QY 541 tcaagttttaaactcgtagaagtttaacccaagaacaaagttccttataatgaactc 600
DB 541 TCAAGTTTAAAACTGTAGAAAGTTAACCCGAAGAACAGTTGCTCTTATTAATGAACCTC 600
QY 601 tgggttcaacccggttgccaaaggctggaacttactcaataaatttgcactaga 660
DB 601 TCGGGTTCAACCGGTTTGGCCAAAAGGTGCAACTTATCATGAATGCAAGTCACCTAGA 660
QY 661 ttcttcacgctagagatccaatttatggaacaaagtttcacaaagccagctatttta 720
DB 661 TTTTTCACGCTTAGATATCAATTTATGGAACCAAGTTTACACAGCAGCGCTATTTTTA 720
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DB 721 ACTGTATGACCATTTCCATCATGATGTTTGGTATGTTACTTATAGGCTATATCACTTGT 780
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DB 901 GAATTACTCGAATAATATATATTTATCAAAATTTAGTTGAATTCATCTGGCGAGCACCT 960
QY 961 ttatctaaagaatttggtaagctgtgtgtagaactttaaattaccgggtgtgtcaca 1020
DB 961 TTATCTAAAGAAATTTGTAAGCTGTGTGCTAGACGTTTAAATTTACCGGCTGTCTCA 1020
QY 1021 gctatggtttaacagaacaaactctgcaattatatacaccggaagcgatgataa 1080
DB 1021 GCGTATGTTTAAACAAACAACTCTGCAATTTATATACACACGGAAGCATGTTAA 1080
QY 1081 ccaagtgcttcctgcaagctgtgcattatttaaagcaaaagtatcgacttgact 1140
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DB 1141 AAAAAAATTTGGCCCGAAGACGCTGGAAGATTTGTTAAAGGCTCTATGCTTATG 1200
QY 1201 aaggttactatgaataatccagaagcaacaagaagaatcatagatgaagaagttgtg 1260
DB 1201 AAAGGTTATGATATATATCAGACAGCAACAGAAATATATGATGAAGAGTTGTTG 1260
QY 1261 caacacagagataatggtgattacgaatgaagaaaaaacttcttactcgltgacgttg 1320
DB 1261 CACACAGGAGATTTGGGATTTACGATGAAGAAAAACATTTCTTATTCGTGATCGTTG 1320
QY 1321 aaggtcttaatacaaaagaagatatacaagtaacacccgtcgaatttaaatctgtct 1380
DB 1321 AAGGCTTTATATCAATACAAAGGATATCAAGTACACCTGTGAATTAAGATCTGTTCT 1380
QY 1381 ttgcaacatccaataattttttagtcgcgctgtgtcgtggttcagatccctatactgt 1440
DB 1381 TTGCAACATCAAAATATTTTATGATGCGCGCTTGTGCGCTTCAGATCTTATAGTGTG 1440
QY 1441 gagcttcggagagctgtgtgttacttaagaagaagaatactatgactgaaagaagta 1500
DB 1441 GAGCTTCCGGGAGCTGTGTTGTACTTGAAGAAAGCAAAATCTATATGCAAAAGAGTA 1500
QY 1501 atggaattacgttgcagtaagtttcaaatgcaaacgtttgcgtggtgtgttccgtttt 1560
DB 1501 ATGGAATTACGTTGCTAGTCAAGTTTCAAAATGCAAAACGTTTCCGTGCTGTGCTGTTT 1560

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Oy 1561 gtggacgaagtacctaaagctcaccggtgaaattgcaggtgaaacagcttggaaata 1620
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Db 1561 GTGACGAAAGTACCTTAAAGGCTCAGTGGTAAATTGACGGTAAAGCAATTGAGCAATA 1620
      |||||||

Oy 1621 ctgaagaaccagttgctaagatg 1644
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Db 1621 CTGAAGAACCAGTTGCTAGATG 1644

RESULT 4
US-08-460-934-8
: Sequence 8, Application US/08460934
: Patent No. 5814465
: GENERAL INFORMATION:
: APPLICANT: TATSUMI, HIROKI
: APPLICANT: FUKUDA, SATOSHI
: APPLICANT: KIKUCHI, MAMORU
: APPLICANT: KOTAMA, YASUJI
: TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
: TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A
: TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINYLATED AND A BIOLUMINESCENT
: TITLE OF INVENTION: ANALYSIS METHOD
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
: ADDRESSEE: P.C.
: STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
: CITY: ARLINGTON
: STATE: VA
: COUNTRY: USA
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/460,934
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 193798/1994
: FILING DATE: 27-JUL-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 54625/1995
: FILING DATE: 14-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 98857/1995
: FILING DATE: 24-APR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: OBLON, NORMAN F.
: REGISTRATION NUMBER: 24,618
: REFERENCE/DOCKET NUMBER: 7126-001-0
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-413-3000
: TELEFAX: 703-413-2220
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1908 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: unknown
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..1908
: OTHER INFORMATION: /note= "The nucleotide sequence of
: OTHER INFORMATION: the biotinylated firefly luciferase gene contained in
: OTHER INFORMATION: recombinant plasmid pHLf248 DNA"
: NAME/KEY: CDS
: LOCATION: 1..1908
US-08-460-934-8

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US-08-782-118-8
Sequence 8, Application US/08782118
Patent No. 5843746
GENERAL INFORMATION:
APPLICANT: TATSUMI, HIROKI
APPLICANT: FUKUDA, SATOSHI
APPLICANT: KIKUCHI, MAMORU
APPLICANT: Koyama, Yasuji
TITLE OF INVENTION: BIOTINATED FIREFLY LUCIFERASE, A GENE
TITLE OF INVENTION: FOR BIOTINATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A
TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
TITLE OF INVENTION: ANALYST METHOD
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/782,118
3 FILING DATE: 13-JAN-1997
4 CLASSIFICATION: 435
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: US 08/460,934
7 FILING DATE: 05-JUN-1995
8 APPLICATION NUMBER: JP 193798/1994
9 FILING DATE: 27-JUL-1994
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: JP 54625/1995
12 FILING DATE: 14-MAR-1995
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: JP 98857/1995
15 FILING DATE: 24-APR-1995
16 ATTORNEY/AGENT INFORMATION:
17 NAME: OBLON, NORMAN F.
18 REGISTRATION NUMBER: 24,618
19 REFERENCE/DOCKET NUMBER: 7126-001-0
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: 703-413-3000
22 TELEFAX: 703-413-2220
23 INFORMATION FOR SEQ ID NO: 8:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 1908 base pairs
26 TYPE: nucleic acid
27 STRANDEDNESS: double
28 TOPOLOGY: unknown
29 MOLECULE TYPE: DNA (genomic)
30 FEATURE:
31 NAME/KEY: misc.feature
32 LOCATION: 1..1908
33 OTHER INFORMATION: /note="The nucleotide sequence of
34 OTHER INFORMATION: the biotinylated firefly luciferase gene contained
35 OTHER INFORMATION: recombinant plasmid pHLf248 DNA"
36 FEATURE:
37 NAME/KEY: CDS
38 LOCATION: 1..1908
39 IS-08-782-118-8

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US-08-460-934-5
Sequence 5, Application US/08460934
Patent No. 5814465
GENERAL INFORMATION:
APPLICANT: TATSUMI, HIROKI
APPLICANT: FUKUDA, SATOSHI
APPLICANT: KIKUCHI, MAMORU
APPLICANT: KOYAMA, YASUJI
TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A
PROCESS FOR PRODUCING BIOTINYLATED AND A BIOLUMINESCENT
TITLE OF INVENTION: ANALYSIS METHOD
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,934
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 193798/1994
FILING DATE: 27-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54625/1995
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 98857/1995
FILING DATE: 24-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7126-001-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1704 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1704
FEATURE:
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OTHER INFORMATION: /note="Nucleotide sequence of the

OTHER INFORMATION: biotinylated firefly luciferase gene contained in recombinant
; OTHER INFORMATION: plasmid pHLf203 DNA*
US-08-460-934-5

Query Match 98.7%; Score 1622.8; DB 1; Length 1704;
Best Local Similarity 99.6%; Pred. No. 0;
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OY 671 ctgaagatccaattatagaacaaagggttccacgaagaatgataatgataatgata 730
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 731 ctgaagatccaattatagaacaaagggttccacgaagaatgataatgataatgata 790
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 731 catccatcatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 790
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Db 791 catccatcatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 850
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OY 791 ttgtcatgttgaagaatgtgacgaagaatgtttaaagaacatgcaagaatgataat 850
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Db 851 ttgtcatgttgaagaatgtgacgaagaatgtttaaagaacatgcaagaatgataat 910
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OY 851 gttcgaagcgttatctgtgacgaactgtgtgtcaacttctatagaagaatgataat 910
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Db 911 gttcgaagcgttatctgtgacgaactgtgtgtcaacttctatagaagaatgataat 970
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OY 911 ataataatgataatgataatgataatgataatgataatgataatgataatgataat 970
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Db 971 ataataatgataatgataatgataatgataatgataatgataatgataatgataat 1030
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OY 971 aaattgtgaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1030
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Db 1031 aaattgtgaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1090
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1031 taacagaacaaacccctgtcaattatatacaccggaagaatgataatgataatgata 1090
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Db 1091 taacagaacaaacccctgtcaattatatacaccggaagaatgataatgataatgata 1150
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OY 1091 ctggaacaaagttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1150
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Db 1151 ctggaacaaagttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1210
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OY 1151 tgggcccgaacacagctgtgaagaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1210
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1211 tgggcccgaacacagctgtgaagaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1270
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1211 taagataatccagaagaacagaagaatataagaagaatgtgtgtgtgtgtgtgtgt 1270
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1271 taagataatccagaagaacagaagaatataagaagaatgtgtgtgtgtgtgtgtgt 1330
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OY 1271 atattgtgtatagcgtatgaagaagaacattcttatacgtgtgtgtgtgtgtgtgt 1330
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Db 1331 atattgtgtatagcgtatgaagaagaacattcttatacgtgtgtgtgtgtgtgtgt 1390
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OY 1331 tcaatacaagaagatatacgaatccacccctgtcaatgataatgataatgataatgata 1390
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Db 1391 tcaatacaagaagatatacgaatccacccctgtcaatgataatgataatgataatgata 1450
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OY 1391 caaatattttgtatgcgcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1450
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Db 1451 caaatattttgtatgcgcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1510
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OY 1451 gaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1510
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Db 1511 gaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1570
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OY 1511 ttgctagcaagtttcaaatgacaaacagttgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1570
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Db 1571 ttgctagcaagtttcaaatgacaaacagttgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1630
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OY 1571 tacttaagtgctcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1630
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Db 1631 tacttaagtgctcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1690
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OY 1631 caatgtgtaaatgt 1644
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1691 caatgtgtaaatgt 1704
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RESULT 7
US-08-782-118-5
; Sequence 5, Application US/08782118
; Patent No. 5843746
GENERAL INFORMATION:
APPLICANT: TATSUMI, HIKOKI
APPLICANT: FUKUDA, SATOSHI
APPLICANT: KIKUCHI, MAMORU
APPLICANT: KOYAMA, YASUJI
TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A
TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINYLATED AND A BIOLUMINESCENT
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

Db 1141 AAAAATCTTAGCTCTTAACAGACGTGAGAACTTTGTGTTAAAGACCTATCTTATG 1200
Qy 1201 aaaggtatagatagatccagaagcacaagaagaatcctagatgagaagtgcttg 1260
Db 1201 AAAGGTATGTAATTAATCCAGAGCAAAAGAACTTATGAGAGAAAGGTTGGCTG 1260
Qy 1261 cacaagaagatctggtatctagatgaagaacacattcttactcgtgagatcgttg 1320
Db 1261 CACACCGAGATATTGATATATGATGACAAACAACTTTCTTATTTGCGATCGTTTG 1320
Qy 1321 aagctttaaatacaatacaagaagatcaagtaaccctcgtgaatagaatcgttctt 1380
Db 1321 AAGCTTAAATCAATACAAAGAGATACCAAGTACCACTGCGCAATTAAGATCCGTTCTT 1380
Qy 1381 ttgacaatcccaatatttttgatgacgagcggttgctgcttcagatcctatagcgtg 1440
Db 1381 TTGGACATCCATCTATCTTATGATGCTGCTTGCAGCTCTCTGATCCGTGAGCTGGC 1440
Qy 1441 gagctccgagagctgtgtgttacttaagaagaagaatctagactgaagaagaagta 1500
Db 1441 GAGCTTCAGAGACCGCTTTGTTGTACTGGAAGCGAAAAAATATGACCGAAAAAGAGTA 1500
Qy 1501 atgattacgttgctgaagttcaaatgcaaacgcttgctgctgctgctgctt 1560
Db 1501 ATGATTAATGTTGCAAGTCAAGTTTCAAAATGCAAAAGCTTACGCTGCTGCTGCTTTT 1560
Qy 1561 gtgagcgaagtaactaaagctcactcgtgtaaaatlcagcgttaagaacatlagagaata 1620
Db 1561 GTGATGTAAGTACTAAAGGCTTACTGGAATAATTGACGCGAGAGAAATTAGAAGAAATC 1620
Qy 1621 ctgaagaacaacagttgctgaagatg 1644
Db 1621 CTTAAGAAACAGTGTCTAAGATG 1644

RESULT 9
US-07-903-047-1
Sequence 1, Application US/07903047
Patent No. 5229285
GENERAL INFORMATION:
APPLICANT: Kajiyama, Naoki
APPLICANT: Nakano, Eiichi
TITLE OF INVENTION: Thermostable Luciferase Of Firefly.
TITLE OF INVENTION: Thermostable Luciferase Gene Of Firefly, No. 5229285el Recombi
TITLE OF INVENTION: DNA, And Process For The Preparation Of Thermostable
TITLE OF INVENTION: Luciferase Of Firefly
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,047
FILING DATE: 19920623
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 863-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1644 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA to mRNA
US-07-903-047-1

Query Match 82.5%; Score 1356; DB 1; Length 1644;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

Qy 1 atggaagaacatgagagacatgaaatattgltatgctcgaaccatttaccctatt 60
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Qy 121 gcaattgctttactaagcacttaccggtgtcgaattatagtaagcgaactatga 180
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Qy 181 aaatcagctgcttagagagagccttaagaagaatcgtgttgcttgatggaagaat 240
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Qy 241 gcgtatgacgtgaagaacttcttattcctgtaattagcggcttattata 300
Db 241 GCCTTATGCGTGAAGAACTGTGAAGAAATTTTATTCCTGTAATACCGCGACTGTTTATA 300
Qy 301 ggtgtcgtgtggtcccaataatgaaatgtaacctcagcgtgaattgttcaagttta 360
Db 301 GGTGTGCTGTGTCACCCACTAATGAGATTTACACTTACGTAACGTGTTACACTTTTA 360
Qy 361 ggcactcctaaagcacaacattgattagttcctaaagaagatataagaatttaact 420
Db 361 GGTATCTCTTAACCAACCAATTTGATTTAGTTCTAAAAAAGCGCTTAGATTAAGTTATACA 420
Qy 421 gtacaaagaacggtlaactgctatlaaacaattgtatataatgacagcaaatgtaatt 480
Db 421 GTACAGAAACACTACTACTATTAACCATGTTATTAAGTATGACAGTGTATAT 480
Qy 481 agaggtatcaatccatgagcaacttataaaaaaacacacacacaggtttcaagga 540
Db 481 CGAGGATATCAATGCTGACACCTTTATAAAAAGAAACACTCCACAGGTTTTCAMGCA 540
Qy 541 tcaagtttaaacctgtagaagtttaacgcaagaacaggtgtccttataatgaactct 600
Db 541 TCCAGTTTCAAAACGTGTGAGAGTTCACCGTAAGAACAGATGCTTTTAAATGAACCT 600
Qy 601 tccggttcaacggttctgcacaaagggtgtgcaacttactcactgaataattggtlca 660
Db 601 TCGGTTTCTTACCGGTTTGGCAAAAGCGTACAACTTACAGCAAAATACAGTACTACA 660
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Qy 721 acgtgtagcacttccatcactatggtttgttgaatgtaacttaagtcactgaactgt 780
Db 721 ACTGTGCTTCATTCATCATCTGCTTTGATTTGATTTACTACTACTAGAGTATTTAATTT 780
Qy 781 ggttcgtatgtlcaatgtaacgaaatttgacgaagaagactttttaaacaactgtcaa 840
Db 781 GGTTCGTGTGTGTAATGTTAAACAAATTCGATGAGAAACATTTTAAACCTGTACAA 840
Qy 841 gattcaaaatgtcagaagcgttattcttgtaacgacttgttgcaattccttaataaga 900
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||||| 181 NAATCATGTTGCTGTAAGAAAGCTTGCAAAATATGTTGGTTGTATGTCAGCAAT 240
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QY 301 ggtgtcgt 360
Db 301 GGT 360
QY 361 ggcattccaaagccaaactgttatttgccttcaaaaagagattagataagttataact 420
Db 361 GGTATGTCATAAACCACAACTGTATTTAGTTCATAAAGGCTTACATAAGTTATATACA 420
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Db 421 GTACAAAACACAGTACTACTATTAAACCATTTGTATAGTATAGCAAAAGTTGATTA 480
QY 481 agaggttataatccatgagcaacttattataaaaaaacctccaaagttccaagta 540
Db 481 CAGGATATCAATGCTGTGACACCTTTATATAAAGAAACCTCCACGAGTTTCAAGCA 540
QY 541 tcaagtttaaaactgtagaagttaaacgaaagacagtgctcttataaagtaactc 600
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QY 661 tttctcagcgttagagatccaaattttagaagaaagattccaccaggtcagcagctattta 720
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QY 901 gaattactcgaataatagattatcaaatltagltgaaltgtgacatctgagcagacact 960
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QY 1021 ggcattggtttaaacaagaacactctgcattatataccaccggaagacgagatgataa 1080
Db 1021 GGTATGTTTAAACACAAACATCTGCATTTATTTACACAGAGAGAGAGATGATAA 1080
QY 1081 ccaagtgcttctggaagatgtgtccattatttaaagcaaaagttatcgatctgatact 1140
Db 1081 CCAAGGAGCTTCTGAAAGAGCTGCGCTGTTTAAAGCAAAAGTTATGATCTTGATATCC 1140
QY 1141 aaaaaaaccttggcccggaacagcgtgagaaagttgtgtaaggttccatgctatgt 1200
Db 1141 AAAAAAATCTTTAGGCTTAAACAGCGTGAGAGGTTGTGTTAAAGGACCTATGCTTATG 1200
QY 1201 aaaggtatgataataccagaagaacaagaagaatcatalagatgaagaaggtgtgt 1260
Db 1201 AAAGGTTATGTAATATATCCAGAGCAACAAAGAACTTTTACGAGAGAGAGGTGGCTG 1260
QY 1261 cacacagagatatgtgattacgaatgaagaanaaacatttcttactcgtgagctgtgt 1320
Db 1261 CACACGAGAGATATGGAATATGATGAGAGAAACATTTCTTATGTCAGTCGTTTG 1320

Db 1261 CACACGAGAGATATGGAATATGATGAGAGAAACATTTCTTATGTCAGTCGTTTG 1320
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QY 1441 gaagcttcggagcgt 1500
Db 1441 GAGCTTCCAGAGACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
QY 1501 atgattacgt 1560
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QY 1561 gtgacgaagttacctaagttcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1620
Db 1561 GTGATGAGAGTACCTTAAGTCTTACTGTGAAAAATTTACGCGACAGACGAATTAAGAAATC 1620
QY 1621 ctgaagaacacagttgtctaagatg 1644
Db 1621 CTTAAGAAACCACTGCTAAGATG 1644

RESULT 12
US-09-447-208-3
Sequence 3, Application US/09447208
Patent No. 613886
GENERAL INFORMATION:
APPLICANT: Bryan, Bruce
TITLE OF INVENTION: BIOUMINESCENT ARTICLES OF MANUFACTURE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McNuliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/447, 208
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0909/135, 988
FILING DATE: 08-17-98
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/757, 046
FILING DATE: 11-25-96
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/597, 274
FILING DATE: 02-06-96
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24727-105C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-450-8499
TELEX:
INFORMATION FOR SEQ. ID NO.: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1644 base pairs

QY 1501 atggattacgttgctagtcgaagtttcaaatgcaaaacgtttgctggtgctcgtttt 1560
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Db 1501 atggattacgttgctagtcgaagtttcaaatgcaaaacgtttgctggtcgtttt 1560
QY 1561 gtcgaagaagtaactaaagctcactcgtgtaaaatgacgttaagcaatlaagaata 1620
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1561 gtcgaagaagtaactaaagctcactcgtgtaaaatgacgttaagcaatlaagaata 1620
QY 1621 ctgaagaacacagttgctgaagtg 1644
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1621 ctgaagaacacagttgctgaagtg 1644

RESULT 15
US-08-597-274A-3
; Sequence 3, Application US/08597274A
; Patent No. 6247995
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; TITLE OF INVENTION: BIOLUMINESCENT NOVELTY ITEMS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/597, 274A
; FILING DATE: 02/06/96
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6680-105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1644 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1644
; OTHER INFORMATION: Luciola Cruciata Luciferase (Firefly)
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: 4,968,613
; US-08-597-274A-3

Query Match 82.5%; Score 1356; DB 4; Length 1644;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 164; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 61 gaagaggatctgctgagacaaattgcgaagtatatgatcatgatgcaaaacttgga 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GAAGAGGATCTCTGGAACACAAATTACGCAATTACATGAGGATATGCAAACTTGGC 120
QY 121 gcaatgcttcttaactaaagcactaccgyltgcattatatacgaacgaacttaaga 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GCAATGCTTTTACAAATGACATTACTGGTGTGATTATCTTACCCGAACTTGGAG 180
QY 181 aaatcatgctgcttaagagagagctttaaagaatataggttggttgttgatgaaga 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 AAATCATGTTGTAGCAAAAGCTTTGCAAAATTAATGCTTGGTTGTGATGCGCAGAA 240
QY 241 gcttatcgatgaagaacttgagaattctctattcctgattatgaacggtattatata 300
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 GCCTTATGCACTGAAAACCTGAGAAATTTTATTCCTCTATATACCGGACCTTTATA 300
QY 301 ggtgctggtgctgctcgaactaagatgacattacacctcagatgaattgltcagat 360
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QY 361 ggcattcttaagcgaacaaattgattagttcttaaaagagatgaataaacttaact 420
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QY 421 gtacaaaacagtgtaactgctatataaacattgtatatttgacagcaagtgatatt 480
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QY 481 agaggtatcaatccatggaacattatataaaaaaacatccacaaggttccaagga 540
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Db 481 CGAGGATATCAATGCTGACACCTTTATTAATAAAGAAACCTCACACAGGTTTCAAGA 540
QY 541 tcaagttttaaactctagaagtttaacccgaagaacaaattgctctataagaactc 600
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QY 601 tcggttccaacggttctgcacaaagggtgtaacttaactactaagaattgtgcactaga 660
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QY 661 tttctcaagctagaagatccaatltatggaacccaagttccacgaagcgctatttta 720
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QY 721 actgtatgacattcacaatggttggatgttgaatttacttaacttaagcttaactgt 780
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Db 721 ACTGTGTTCCATTCCATCATCTGTTTGGTATGTTCATCTACTAGGATTTTAAATTTGT 780
QY 781 ggttcgtatgtcaltgtaagaaatttgacgaagagactttttaaaacatlgcaa 840
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QY 841 gattacaatgttcaagcgttaltcttgtaacgaactgttgcaattccttaagaagt 900
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QY 901 gaattactgataatataatgattatatacaattgtgaattgcaattgcatctgcggaagc 960
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QY 1081 ccagtggtcttgcaagatgtgccaattatataaagcaaaatgttcgaattgcttact 1140
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Db 1141 AAAAAATCTTAGCTCCTAACAGACGTGAGAAAGTTGTGTTAAGAGACCTATGCTTATG 1200
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QY 1261 cacaagaagaatattggtatcacgaagaagaacattcttctatcgtlgaatcgttg 1320
Db 1261 CACACCGAGATATTGATATATGATGAGAAAAACATTTCTTATTGTGATCGTTTG 1320
QY 1321 aagtccttaatacaatacaagaatatacaagtaaccactgtgaattagaatctgttct 1380
Db 1321 AAGTCTTAATCAATAATACAAAGATACCAAGTACCACTGCGCAATTAGAAATCCGTTCTT 1380
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QY 1441 gagctccggagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1500
Db 1441 GAGCTTCCAGAGAGCCGTTGTTGTACTGGAAGCCGAAAAAATATGACCGAAAAAGAGTA 1500
QY 1501 atggaatacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1560
Db 1501 ATGATTTATGTTCAGAGTCAAGTTTCAAAATGCAAAACGTTTACGTGTGTGTGTGTGT 1560
QY 1561 gtgagcgaagtaactaaagctcactcgtgttaaatltgacggttaagcaattagaagaata 1620
Db 1561 GTGATGTGAAGTACTTAAAGCTTACTAGGAATAATGACGCGAGAGCAATTAGAGAAATC 1620
QY 1621 ctgaagaacaacagttgtctaagatg 1644
Db 1621 CTTAAGAAACCACTTGTCTAAGATG 1644
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Search completed: September 6, 2002, 19:29:53
Job time: 15156 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 15:07:47 : Search time 3537.97 Seconds
(without alignments)
6271.674 Million cell updates/sec

Title: US-09-581-241-3
Perfect score: 1644
Sequence: 1 atggaacacatgagagacga.....aggaaccatgtgctaagatg 1644

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estdb:*
2: em_esthum:*
3: em_estnu:*
4: em_estov:*
5: em_estpl:*
6: em_estro:*
7: em_estro:*
8: em_hic:*
9: qb_est1:*
10: qb_est2:*
11: qb_hic:*
12: qb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	208.6	12.7	664	10 C83857	C83857 C83857 Dict
2	199.4	12.1	768	10 BM412281	BM412281 EST586608
3	198.2	12.1	667	9 A1486799	A1486799 EST245121
4	190.4	11.6	651	10 C90519	C90519 C90519 Dict
5	189.8	11.5	582	9 AM621420	AM621420 EST312218
6	185.8	11.3	625	9 A1485586	A1485586 EST243907
7	183.2	11.1	569	9 AM218471	AM218471 EST303654
8	181.6	11.0	522	9 A1488821	A1488821 EST247160
9	173.8	10.6	543	10 BE555239	BE555239 sp87a10.y
10	173.6	10.6	612	10 BG130292	BG130292 EST475938
11	171.8	10.5	606	10 B1923203	B1923203 EST543107
12	165.6	10.1	741	9 AU214129	AU214129 AU214129
13	162.4	9.9	535	9 A1389862	A1389862 MTRC57H09
14	162.2	9.9	498	10 B1425803	B1425803 sah72f03.
15	162.2	9.9	570	10 BG791252	BG791252 ESTFNL115
16	161.4	9.8	548	10 BM188336	BM188336 sa199f03.
17	159.4	9.7	604	9 AU219684	AU219684 AU219684

18	159.4	9.7	604	9 AV558307	AV558307
19	158.8	9.7	520	10 B1269977	B1269977 NF003D02F
20	158.8	9.7	638	9 AU214473	AU214473 AU214473
C 21	158.2	9.6	712	9 AM349844	AM349844 GM210006A
C 22	158	9.6	611	10 B129072	B129072 B129072
C 23	157.8	9.6	644	10 B1309413	B1309413 EST330823
C 24	157.8	9.6	722	10 B139943	B139943 B139943
C 25	157.6	9.6	590	9 AM329421	AM329421 N2006566
C 26	157.4	9.6	558	9 AV680337	AV680337 AV680337
C 27	157.4	9.6	567	10 BG580544	BG580544 EST482271
C 28	157.4	9.6	656	9 AM691106	AM691106 NF041C08S
C 29	154.8	9.4	410	10 BM109695	BM109695 EST557231
C 30	154.8	9.4	977	12 CNG01MDU	AL150803 Anopheles
C 31	152.2	9.3	808	9 AM34381	AM34381 GM210002A
C 32	150.2	9.1	540	9 A1771202	A1771202 EST252398
C 33	149.6	9.1	506	9 AM132800	AM132800 sei0411.y
C 34	149.2	9.1	529	10 BM143081	BM143081 sb56d11.y
C 35	148.8	9.1	377	9 A1938631	A1938631 sb56d11.y
C 36	148.8	9.1	655	9 AM560940	AM560940 EST315988
C 37	148.6	9.0	453	10 BF005122	BF005122 EST433620
C 38	148.6	9.0	495	9 AU284477	AJ284477 AA38-AA-X
C 39	147	8.9	508	9 AM423914	AM423914 sh57907.y
C 40	146.2	8.9	683	10 BF492687	BF492687 AT01136.3
C 41	145.8	8.9	565	10 BE330067	BE330067 so73a05.y
C 42	145.8	8.9	665	10 BF200141	BF200141 WHE2252.E
C 43	145	8.8	595	9 AM329094	AM329094 N2003006
C 44	144.6	8.8	623	10 BF634495	BF634495 NF062809D
C 45	144.4	8.8	501	10 BG882703	BG882703 sae51e04.

ALIGNMENTS

RESULT 1
C83857
LOCUS C83857
DEFINITION C83857 Dictyostellium discoideum ss (H. Urushihara) Dictyostellium
ACCESSION C83857
VERSION C83857
KEYWORDS C83857.1 GI:2706789
SOURCE Dictyostellium discoideum.
ORGANISM Dictyostellium discoideum
REFERENCE 1 (bases 1 to 664)
AUTHORS Morio,T., Urushihara,H., Saito,T., Ugaawa,Y., Mizuno,H., Yoshida,M.,
Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H.,
Williams,J., Maeda,M., Takeuchi,I., Ochiai,H., and Tanaka,Y.
The Dictyostellium developmental cDNA project: generation and
analysis of expressed sequence tags from the first-finger stage of
development
DNA Res. 5 (6), 335-340 (1998)
MEDLINE 99156227
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402huesakura.cc.tsukuba.ac.jp
PROJECT = "Dictyostellium discoideum cDNA project in Japan"
POLYA=No.

FEATURES
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/strain="AX4"
/db_xref="taxon:44689"
/clone="SSA391"
/clone_idb="Dictyostellium discoideum ss (H. Urushihara)"
/dev_stage="slug"

BASE COUNT 234 a 105 c 124 g 201 t
ORIGIN

Query Match 12.7%; Score 208.6; DB 10; Length 664;

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QY	1237	atcatagatgaagaagtgcttggttcacacacaggaatatttggtatctaagaiaaagaaaaa	1296
Db	120	GTCATAGATTAAGATGAGTATCTTTAAAAACGTGTATATGGTTATGTTGATMAATGGT	179
QY	1297	catcttcctatcgttgagtcggttgaagtcctttaaccaatacaagaagatcatcaagtaacca	1356
Db	180	TATTTCTTTATCATCGATATGATCAAAAGCAATTTGATCAAAATGTAAAGGTTTCCAAAGTACCA	239
QY	1357	ccgtgcgaatgaagatcctgcttccttttgaacataccaatlatlttgaigcgcgcgttgct	1416
Db	240	CCTGCTGATTAAGAGCACTTACTATTATTCATCCAAAGTGCAGATGCCGTGTAGTA	299
QY	1417	ggcgcttccagatcccatatgcctggtgtagcttccgcggagctgctggttacttaagaagaaga	1476
Db	300	GCTCTTTTAAAAAGGATGATGGGTAAAGTACCAACAGGCTTCGTGTTATTAACAAAAAT	359
QY	1477	aaatcctgactgaagaaagaagtaatggatcagcttgctagtcgaagtttcaaatgcaaaa	1536
Db	360	GAATCTCTTACTGAAAAAAGAACTCTTGGATTTGGGCTCACCCAAAATTTGCCAATTTATATAA	419
QY	1537	cgtttgcgttggtgctgccttcttggttggacgaagtaactcaaaagtcactggttaaat	1596
Db	420	CATTTCAGAGGTGGTATCTTTTTCATACCTGCATTTCCTAATCTGCAACTGTTAAACTA	479
QY	1597	gaacgttaagaacattagaga	1616
Db	480	TTACGCTAAAAATCTTTAAAGA	499

RESULT	5
LOCUS	AM621420 582 bp mRNA linear EST 18-MAY-2001
DEFINITION	EST312218 tomato root during/after fruit set, Cornell University
ACCESSION	LYopersicon esculentum cDNA clone CLEX11N8 5', mRNA sequence.
VERSION	AM621420
KEYWORDS	AM621420.1 GI:7333067
SOURCE	EST.
ORGANISM	tomato.
REFERENCE	LYopersicon esculentum
AUTHORS	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; easterids I; Solanales; Solanaceae; Solanum;
	LYopersicon.
	1 (bases 1 to 582)
	van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Kochian,L., Liang,F., Hansen,T., Craven,M.B., Bowman,C.L., Roming,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
TITLE	Generation of ESTs from tomato root, during and after fruit set
JOURNAL	unpublished (1999)
COMMENT	Contact: CUGI
	Clemson University Genomics Institute
	Clemson University
	100 Jordan Hall, Clemson, SC 29634, USA
	Email: http://www.genome.clemson.edu/orders/index.html
	5 prime sequence.
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	/cultivar="F4A96"
	/db_xref="taxon:4081"
	/clone="CLEX11N8"
	/clone_lib="tomato root during/after fruit set, Cornell University"
	/tissue_type="root"
	/dev_stage="plants during and after fruit-set"
	/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Tanksley; Tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY 14850)."
BASE COUNT	181 a 99 c 146 g 156 t
ORIGIN	

Query Match	11.5%	Score 189.8	DB 9	Length 582
Best Local Similarity	60.6%	Pred. No. 2.7e-33		
Matches 330	Conservative 0	Mismatches 212	Indels 3	Gaps 1

OY	1079	aaagggggtcttcgtgcgaagaagtgtgccattatttaagcaaaagttacgctcttgata	1138
Db	2	AATCAGGGGCGCATGTGCTACCGTTTGAGAGAACGCAGAGATGAAATAATTGTGGATCCGGATA	61
OY	1139	ctaaaaaacatttggccccaagacagacgltvgaaagtgtgtgtaaaagggtcctatgctta	1198
Db	62	CGGGTTCCTCTCCGCCCGTAACCAACCOCGGGAATTTTCATTTGAGGTGATCAAAATCA	121
OY	1199	tgaaggttatgtagataaatccagaagacaagaagaatacatagatgaagaagtttgt	1258
Db	122	TGAAGGTTTACTTGAATGACCTTGAAAGCTACAGCTAGAACAAATTAGMAAAGAAGATGCT	181
OY	1259	tgcacacagagatatitggtatlaacgatlgaaagaaaacatttcttaatcgltgagct	1318
Db	182	TACACACTGGCGATWTGGATWATTTGACGATGATGATGATGATGATGATGATGATGAT	241
OY	1319	tgaactcttaatacaataaagaagatatcaagtcaccctgcctgaatgaatgcgtc	1378
Db	242	TGAAGGAATGTGATCAAAATACAAGGATTTTCAAGTGGCGCTCTGTAAGTCAAGCACCTTC	301
OY	1379	ttttgcaacatccaataatlitttgaatgcgcgagctgtgctgtccagatcctaagctg	1438
Db	302	TTGTCAACCCACCCCTTAACATTTCTGTGATGCTGCTGTGCTCAATGAAGATGAACACGG	361
OY	1439	gtgagcttcgcggagctgttftfracttaagaagaagaacatctagatgaagaagaag	1498
Db	362	GAGAGCTTCACATGGCTTTTGTGTAGATCAAAATGATCTACCATTTACTGAGATGAAG	421
OY	1499	taatgattacgtgtcagtcagtcagttlccaalgcaaaaacglttgcgtgtgtgcgt	1558
Db	422	TGAAGGATTTTCAATCCCAAGCAGTGATWTTCTAATAAGAAAT---AAAAGCCTGATTTTT	478
OY	1559	ttgtgacgaagtagaccttaaagtlcacgtgcgtgaatgtacgttgaagaatlaagaata	1618
Db	479	TGTGTGAGACGCTACGGAATCTCCATCAGGAAAAATTTTGAAAAAGACTTAAAGACTA	538
OY	1619	tactg 1623	
Db	539	GACTG 543	
RESULT	6		
LOCUS	A1485586	625 bp mRNA linear EST 18-MAY-2001	
DEFINITION	EST243907 tomato ovary, TMU Lycopersicon esculentum cDNA clone		
VERSION	A1485586		
KEYWORDS	A1485586.1 GI:4380957		
SOURCE	EST.		
ORGANISM	Tomato.		
REFERENCE	Lycopersicon esculentum		
AUTHORS	Eukariyola, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	Asteridae; euasterids I; Solanales; Solanaceae; Solanum;		
	Lycopersicon.		
	1 (bases 1 to 625)		
	Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.		
	, Liang,F., Upton,J., Konning,C.M., Craven,M.B., Fujii,C.Y., Bowman,		
	,C.L., Merman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley		
	,S.D. and Giovannoni,J.		
	Generation of ESTs from tomato carpel tissue		
	Unpublished (1999)		
	Contact: CNGI		
TITLE	Clemson University Genomics Institute		
JOURNAL	Clemson University		
COMMENT	100 Jordan Hall, Clemson, SC 29634, USA		
	Email http://www.genome.clemson.edu/orders/index.html.		

Db	Accession	Length	Source	Version	Keywords
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DEFINITION	AM218471	569 bp	mRNA	linear	EST 18-MAY-2001
ACCESSION	EST303654	tomato radicle, 5 d post-imbibition, Cornell University			
VERSION	AM218471	Lycopersicon esculentum cDNA clone cLE2912, mRNA sequence.			
KEYWORDS	AM218471.1	GI:6529345			
COMMENT	EST.				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
ORGANISM	LYCOPERISON ESCULENTUM			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;			
	Lycopersicon.			
	1 (bases 1 to 569)			
	van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Renning,C.M., Fraser,C.W., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.			
	, Generation of ESTs from tomato radicle tissue			
	Unpublished (1999)			
	Contact: CUGI			
	Clemson University Genomics Institute			
	Clemson University			
	100 Jordan Hall, Clemson, SC 29634, USA			
	Email: http://www.genome.clemson.edu/orders/index.html			
	5 prime sequence.			
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	/clone_id="tomato radicle, 5 d post-imbibition, Cornell University"			
	/tissue_type="radicle"			
	/dex_stage="seedlings 5 days post-imbibition"			
	/note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Tanksley; Tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY 14850)."			
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ORIGIN				
Query Match	11.1%; Score 183.2; DB 9; Length 569;			
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Matches 284;	Conservative 0; Mismatches 160; Indels 0; Gaps 0;			
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Db 55	GATATTTAAATCAGGGGCGATGTGTACCTTTGGAGGAACGAGAGATGAATAATTGTGAT 114			
OY 1132	ctgatactaaaaaactcttgccgcgacagctggaagcttgtaaggtcct 1191			
Db 115	CCGGATACGGGTGCTCTCTGCCCCGTACCAACCCGGTGAATTTCATTTAGAGTGAT 174			
OY 1192	atgcctatgaaggctatgtatgaatacagaagaacaagaagaatcatagatgaaga 1251			
Db 175	CAAAATCATGAAGGATTACTTGAATGACCTCGTAGCTACAGTAGAACAATGAAGAAAGA 234			
OY 1252	ggttggtgtgcacacagagagatatgtggtatcagatgaagaagaacatcttcttcgtg 1311			
Db 235	GGATGTGTACACACTGGCGATTTGGATTTATGTGCGATGATGATGATGACCTTTTCATCGG 294			
OY 1312	gatcgtttgaagctcttatacaataaagaagatactcaagtaacacccctgcgtatagaa 1371			
Db 295	GATGATTGAAGGAAATTTATCAATACAAAGGATTTCAAGTGGCCCTGCTCAACTCGAA 354			
OY 1372	tctgtctcttgcacaatcacaatatcttgatgcggcgctgtcgtgcgttcagatccct 1431			
Db 355	GCACCTTCTTGTCAACACACCCATACATTTCTGATGCTGCTGTTGTCCAATGAAGATGAA 414			
OY 1432	atacgtgtgtgagcttcggggagctgtgtgttgaacttaagaagaagaatctatgactgaa 1491			
Db 415	CAACGGGGAGAGTTCCAGTGGCTTTTGTGTGTAGATCAATATGATGTACCATTTACTGAG 474			
OY 1492	aaagaagtaatgataltaagcttgcagtcaagt 1523			
Db 475	GATGAAGTAGAGATTTTCATCTCCAGAGAGGT 506			

LOCUS AI488821 522 bp mRNA linear EST 18-MAY-2001
 DEFINITION EST247160 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
 CLEP18L20, mRNA sequence.
 ACCESSION AI488821
 VERSION AI488821.1 GI:4384192
 KEYWORDS EST.
 SOURCE tomato.
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
 Lycopersicon.
 REFERENCE 1 (bases 1 to 522)
 Alcalá, J., Vrebalov, J., White, R., Matern, A. L., Vision, T., Holt, I. E.,
 Liang, F., Upton, J., Ronning, C. M., Craven, M. B., Fujii, C. Y., Bowman,
 C. L., Nierman, W., Fraser, C. M., Venter, J. C., Martin, G. B., Tanksley,
 S. D. and Giovannoni, J. J.
 Generation of ESTs from tomato carpel tissue
 Unpublished (1999)
 CONTACT: CUGI
 CLEMSON UNIVERSITY Genomics Institute
 CLEMSON UNIVERSITY
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>.
 Location/Qualifiers
 1..522
 /organism="Lycopersicon esculentum"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="CLEP18L20"
 /clone_1lb="Tomato ovary, TAMU"
 /tissue_type="Carpel"
 /dev_stage="5 days pre-anthesis to 5 days post-anthesis"
 /lab_host="XLI-Blue MRF"
 /note="Vector: Bluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI; cLED - Tomato Carpel EST Library; OligodT-primed and
 directionally cloned cDNA in vector Lambda Zap II with 5'
 and 3' ends located at the EcoRI and XhoI sites,
 respectively."
 BASE COUNT 156 a 89 c 133 g 144 t
 ORIGIN

Query Match 11.0%; Score 181.6; DB 9; Length 522;
 Best Local Similarity 62.6%; Pred. No. 2e-31;
 Matches 283; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 1072 gatgataaacccggtgctcttcgcaagtggtgccattatttaagcaaaagtatcgat 1131
 ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 DB 43 GATATTAAATCAAGGCGATGTGTACCGTTGTAGGAACCGAGAGATGAATTTGTGAT 102
 ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 QY 1132 ctgtatactaaacaaacatttgagccgcaagacgtggaagaatttgtaagaagtcctc 1191
 ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 DB 103 CCGGATACGGGTTGCTCTCTGCGCCCGTAACCAACCGCGTGAATTTGCAATAGAGTGAT 162
 ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 QY 1192 atgcttatgaaagttagtagtaataccagaagcaagaagaatacatagatgaagaa 1251
 ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 DB 163 CAATCATGAAGGTTACTTGAATGACCCGTAAGTACACTAGAACCAATAGAAAAAGAA 222
 ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 QY 1252 gtttggttcgacacagagatattggtattagatgaagaagaacatttcttattcgtg 1311
 ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 DB 223 GGATGGTTACACACTGCGCATGTGATATGATGACGATGATGATGAGCTTTTCATCGTG 282
 ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 QY 1312 gatcgcttaagcttaatacaatacaagaatcatcaatcacccctgctgaattagaa 1371
 |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 DB 283 GATCGATTGAAGAAATTGATCAATACAAAGATTTCAACTGCGCCTGCTGACACTCGAA 342
 |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 QY 1372 tctgtctcttggcaacatcaaatatttgatgcccgcgctgctgctgcttcagatcct 1431
 || |||| || |||| || |||| || |||| || |||| || |||| || |||| || ||||
 DB 343 GCACCTCTTGTCACACACACCTTAATTTGATGATGCTGCTGTTCCCAATGAAAGATGAA 402
 || |||| || |||| || |||| || |||| || |||| || |||| || |||| || ||||
 QY 1432 atagctgtgtagcttcgcggagctgtgtgttacttaagaagaagaataatcatgaactgaa 1491
 || || || || || || || || || || || || || || || || || || || || || || || ||

DB 403 CAAGCGGAGAGACTTCACGTGGCTTTGTTAGATCAATGAAATCTACCATTTACTGAG 462
 QY 1492 aaagaagtaatggattacgtgtgtagtaagt 1523
 || |||| || |||| || |||| || |||| || |||| || |||| || |||| || ||||
 DB 463 GATGAAGTGAAGGATTTTCATCTTCAAGCAGGT 494

RESULT 9
 BE555239 543 bp mRNA linear EST 04-DEC-2001
 LOCUS sp87a10.y1 Gm-cl045 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 DEFINITION Gm-cl045-595 5' similar to TR:048868 048868 4-COMARATE:COA LIGASE
 2.; mRNA sequence.
 ACCESSION BE555239
 VERSION BE555239.1 GI:9819726
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 REFERENCE 1 (bases 1 to 543)
 Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna,
 A., Bolla, B., Matra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers,
 Y., Person, B., Swaller, T., Gilbons, M., Pape, D., Harvey, N., Schurk,
 R., Ratter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann,
 R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)
 CONTACT: Shoemaker R./Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800)-533-4363 or contact via email: cou@resgen.com
 High quality sequence stop: 416.
 Location/Qualifiers
 1..543
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl045-595"
 /clone_1lb="Gm-cl045"
 /tissue_type="Hypocotyl, 9-10 day old etiolated seedlings"
 /lab_host="DH10B"
 /note="Vector: BluescriptII SK+; Site_1: EcoRI; Site_2:
 XhoI; this cDNA library was constructed from mRNA isolated
 from etiolated hypocotyl tissue of 9-10 day old seedlings
 of the cultivar Williams 82. Complementary DNA was
 synthesized from mRNA using a primer consisting of a
 poly(GT) primer with a XhoI restriction site. EcoRI
 adapters were ligated to the blunt-ended cDNA fragments
 followed by digestion with EcoRI and XhoI. The cDNA
 fragments were directionally cloned into the EcoRI-XhoI
 restriction site of the Bluescript vector. The ligated
 cDNA fragments were transformed into DH10B host cells
 (Gibco BRL). This library was constructed by Dr. Randy
 Shoemaker."

BASE COUNT 184 a 92 c 130 g 137 t
 ORIGIN

Query Match 10.6%; Score 173.8; DB 10; Length 543;
 Best Local Similarity 59.0%; Pred. No. 1.3e-29;
 Matches 317; Conservative 0; Mismatches 217; Indels 3; Gaps 1;

QY 1093 ggcaagttgtgccattatttaagcaaaagtatcgatcttgatactaaacatttg 1152
 || || |||| || |||| || |||| || |||| || |||| || |||| || |||| || ||

```

/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cP0F29J22"
/clone_lib="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
/notes="vector: pBluescript SK(+); Site.1: EcoRI; Site.2:
XhoI; Small expanding leaves from the growing tip were
taken from greenhouse plants (4-6wks old TA496). Tissue
was immediately frozen in liquid nitrogen."

```

FEATURES	source
LOCUS	B1923203
DEFINITION	B19233203 B19234107 tomato callus lycopersicon esculentum cDNA clone
ACCESSION	GI:16221846
VERSION	1
KEYWORDS	EST.
SOURCE	tomato.
ORGANISM	Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asterridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE	1 (bases 1 to 606)
AUTHORS	Alcala,J., Veybelov,J., White,R., Viston,T., Karamycheva,S.A., Tsai, J., Uteback,T., Van Aken,S., Romling,C.M., Fraser,C.M., Martin J.B., Tanksley,S.D. and Giovannoni,J.
TITLE	Generation of ESTs from tomato callus tissue (2001)
JOURNAL	Unpublished (2001)
COMMENT	Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html This clone is available through the Clemson University Genomics Institute Seq primer: T3. Location/Qualifiers 1..606 /organism="Lycopersicon esculentum" /cultivar="TA496"

DB	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES
Db	100	TTGACAGCATCTCTTGACAGA	81										
RESULT	13												
AL389862		535 bp	AL389862										
LOCUS													
DEFINITION													
ACCESSION													
VERSION													
KEYWORDS													
SOURCE													
ORGANISM													
REFERENCE													
AUTHORS													
TITLE													
JOURNAL													
COMMENT													
FEATURES													
Source													
1. 535													
/organism="Medicago truncatula"													
/cultivar="Jemalong"													
/db_xref="taxon:3880"													
/clone="MtBC57H09"													
/clone_1bp="MtBC"													
/tissue_type="arbuscular mycorrhiza"													
/dev_stage="harvested 3 weeks post inoculation with Glomus intraradices"													
/note="Vector: pBluescript psk. Site_1: EcoRI; Site_2: XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epilobes soil mix; 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LP8). The plants were watered every day and twice a week with a modified nutrient long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using GigaPack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using Exsacit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note : EST may be of fungal origin."													
BASE COUNT													
ORIGIN													
165 a													
103 c													
124 g													
143 t													
Query Match													
Best Local Similarity													
Matches													
293; Conservative													
0; Mismatches													
196; Indels													
3; Caps													
1;													
1115													
aagcaaatgtatcgatcttgatactataaaaactttgagccgacagagctgtgagaag													
1174													
32													
aatcccaaatgtctcagttgcaaacatgcgaatcccttcacacgacatcaattgaggga													

Oy	1175	tttggtaagaaggtcccttgcttaatgaagaagttaaagtagataatcacaagaacaaag	1234
Db	92	tttggcttacgagagacctgttatgatgcgaagatactttaaacattccagAACCAAAAC	151
Oy	1235	aaatcatagatgaagaaggttggtgtcacacagaagataltygglattacgatgaagaa	1294
Db	152	AAACCATTAAATGATCAGGGTTGGACCGCTTACC GGCGCATCTTGATATTTGTATGAAGA	211
Oy	1285	aacattctttatcg tsgatgttgttaagcttcctaataaatacaagaagataaagac	1354
Db	212	GACAACCTATTTTGTCTGGATGAAATAAAGACTATCAAGTAAAGTAATGGATCAAGTGG	271
Oy	1355	caccctgcgaatatagaaactgtctcttttcgaacaalccaataatlittigatbcgcgcgttg	1414
Db	272	CGCCGTGCGAACCTTAGAACACCTTACTAATTTTCATCCGTAATTTTCGATGCCGGGTGA	331
Oy	1415	ctbgcgtccacgaatccatagctgtgtgacgttcocgyagcgtcgttgttgaactaaagaa	1474
Db	332	TTCCGCTTCCTCGATGCCAACAGCTGGCGAGGTTCCAGTTGCTTTGTTGGCTCACTCA	391
Oy	1475	gaaatcctatgactacataaaaagaagaaatgaatgaatcgttctgtagtcaagtlccaalgcaa	1534
Db	392	ATAGCTTGATTAACCTAAGAAGACATCAAGAAATTTTGTAAGCAAAGAGSTTGCACCATMCA	451
Oy	1535	aacgtttgcgttggttggtgtccgttttgytgacgaagtaacctaaagctcactggttaaa	1594
Db	452	AAAGCTGTGC---GGCGAGTCACTTTTATAGAGAAATTCACAAAGTCACCCACGGGAAGA	508
Oy	1595	ttagcaggtaaag 1606	
Db	509	TTTTAAGAAAGT 520	
RESULT 14			
B1425803		498 bp	mRNA linear EST 29-NOV-2001
LOCUS			
DEFINITION	sah72f03.y1 Cm-cl049 glycine max cDNA clone GENOME SYSTEMS CLONE		
ID:	Gm-cl049-4085 5' similar to TR:O48868 O48868 4-COMARATE:COA		
LIGASE 2 :	, mRNA sequence.		
ACCESSION	B1425803		
VERSION	B1425803.1 GI:15203035		
KEYWORDS	EST.		
SOURCE	glycan.		
ORGANISM	glycine max		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Shoemaker,R., Kelm,P., Vodka,L., Expelding,J., Corvett,V., Khanna,		
	A., Bolla,B., Mairra,M., Hillier,L., Kucaba,T., Martin,S., Beck,C.,		
	Wyllie,T., Underwood,K., Steproe,M., Thelsting,B., Allen,M., Bowers		
	,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk		
	,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann		
	,R., Waterston,R. and Wilson,R.		
TITLE	Public Soybean EST project		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-933-4363 or contact via email: ccu@resgen.com High quality sequence stop: 420. Location/Qualifiers 1..498 /organism="Glycine max" /db_xref="taxon:3847" /clone="GENOME SYSTEMS CLONE ID: Gm-cl049-4085"		
FEATURES			
SOURCE			


```

/clone_11b="Gm-cl049"
/tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="3 week old"
/lab_host="DH10B"
/note="vector: Bluescript II SK+, Site.1: EcoRI; Site.2:
XhoI; The Clark NIL was constructed and seed was provided
by Dr. J. Specht, University of Nebraska (Shoemaker and
Specht, 1995). The cDNA library was constructed from mRNA
isolated from whole seedlings of 3 week old greenhouse
grown plants. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site and a 3' anchor. EcoRI adapters were
ligated to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the Bluescript
vector. The ligated cDNA fragments were transformed into
DH10B host cells (GibcoBRL). The library was constructed
in cooperation with Dr. Paul Keim's laboratory at Northern
Arizona University."

```

Query Match	9.9%;	Score 162.2;	DB 10;	Length 498;
Best Local Similarity	60.5%;	Pred. No. 5.9e-27;		
Matches 285; Conservative	0;	Mismatches 183;	Indels 3;	Gaps 1

QY	1159	aacgaagctggagaagcttctgtgtaaaaggtccatctcttatbaaagatctatgaataat	1218
Db	28	AACAACAACGCGTGAATTTCGATTAACAGGACACAAAGGTATGTAAGATATCTTAATGAC	87
QY	1219	ccagaagaacaagaagaatcatalatgaaagaaagcttggctgcacacaagagatatggg	1278
Db	88	CCAGAGCGCTACAGAGACAACTGTAGACAAAGAAAGAGTGTACACACAGACATATTGTGT	147
QY	1279	tattagatgagaagaacaacttctcttatcgtgtgatacgtttgaagtctttaacaaatc	1338
Db	148	TTCAATTGATGATGTGATGAACTCTTCATTGTTGATGGTTAAAGAAATTGTTCAAAATAC	207
QY	1339	aaagatatcaagatcacccatcgtctgaattgaatcctgtctcttttgcacatccaatat	1398
Db	208	AAAGAGATTCCAAGTGGCTCTCGCTGAGGCTTGAAGCATTTGTGATTGCCACCCAAACATT	267
QY	1399	tttgatgcgagcgtctctgtgcgttccaagatcctatagctgtgtgagcttccggagcgtt	1458
Db	268	TCTATATGCTGCCGTTGTAGGCATGAAGAAAGTGCAGGGGAAATTTCCATTGTCATT	327
QY	1459	gttctacttaagaagaagaatactatgactgcgaagaagaagatgattagcttgcagtc	1518
Db	328	GTTGTGAAGTCMAATGGTTCTTGAGATGCCGAGAGTAATCAAGAAATCACTTTCACAA	387
QY	1519	caagtttccaatgcanaaagcttgcgtgtgtgtgtcgtcttcttgtagcgaagtlactaaa	1578
Db	388	CAGGTGTTTTTTTACAAGAGAAATAGGTAGAGTTTTT---TTACAGGACTCTTATTCCTTAA	444
QY	1579	ggtctgactgttaaatatgtccgttlaagcaaatatgagaatcttgaaga	1629
Db	445	GCACCTTCAGGCAAAATTTGCGAAAAGATTTAAGTCGAAGACTTAAACAA	495

RESULT 15	LOCUS	DEFINITION
BG791252	570 bp	mRNA
BG791252		linear
		EST 16-MAY-2001
		EsperN115 Tomato Root Subtraction cDNA Library Lycoposon
		esculentum cDNA clone 10D1 5' similar to 4-coumarate--CoA ligase 2
		, mRNA sequence.

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
BS791252	BS791252.1	GI:14126814	EST.	tomato.
				Lycopersicon esculentum
				Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	COMMENT
	1 (bases 1 to 570)				
	Wang Y.-H., Garvin, D.F. and Kochian, L.V.	Nitrate-induced genes in tomato roots: array analysis reveals novel genes that may play a role in nitrogen nutrition	Plant Physiol.	127 (1), 345-359 (2001)	
	21437959				
	Contact: Kochian LV				

US Plant Soil & Nutrition Lab
Cornell University
Tower Rd., Ithaca, NY 14853, USA
Tel: (607) 255-5445
Fax: (607) 255-1132
Email: lwl@cornell.edu
Seq primer: T3.
Location/Qualifiers

FEATURES	Location/Qualifiers
source	1. .570

```

BASE COUNT      172 a      103 c      136 g      159 t
ORIGIN
/note="Organ: Roots; Vector: pBluescript KS; Directional

```

Query Match	9.9%	Score 162.2	DB 10	Length 570
Best Local Similarity	62.2%	Pred. No. 6.1e-27		
Matches 273	Conservative 0	Mismatches 163	Indels 3	Gaps 1

QY	1185	gggcccatagtcttatataaagattatgtagataatccagaagaacaaagaaatcataga	1244
Db	33	GGGTGATCAAAATATGAAAGGTTACTTTGAACGACCCCTGAAGCTACAGCTAGAACAAATTGA	92
QY	1245	tgaaagaagtttggltgcacacagagatalttggtatlaagatlgagaanaaacattctt	1304
Db	93	AAAAGAGATGAGTTCACACCTGCATCGCATTTGGATATTTCAGACGATGATGACCTTTT	152
QY	1305	tatcttgatccgttttgaagcttctaataatacaagaatatcaagtaaccaaccgtcgtga	1364
Db	153	CATCGTGTGATCGATTGAAGGAATTTGATCAAAATTCAAAGATTTTCAAGTGGCCCTCGTGA	212
QY	1365	atagaatcgttcttcttgcgaacatccaaataatttgaatgcggcggttgcctgagcttc	1424
Db	213	ACTGGAAGCACTTCTGTCTCAACCAACCCCTAAACATTTGATGTGCTGCTGTGCCAATGAA	272
QY	1425	agatccatactcgtgtgtagacctccggagagctgttltgttacttaagaagaataatcat	1484
Db	273	AGATGAACAAGCGGGAGAAATTCACATGGCTTTTGTGTAGATCAAAATGATTCACAT	332
QY	1485	gactgtaaaaagaagtaatgattacglttgtagtcaagtttccaatgacaaacglttcg	1544
Db	333	TACGTGAGATGAGTGAAGATTTTCATCTCCAAACGATGATATTCATTAAGAGAT---	389
QY	1545	tgtgtgtgtcgttcttctgtagaagaagtacctaaagttcactcgtgttaaatltgacgttaa	1604
Db	390	AAAGCCGTATTTTGTGTGGAGACGGTACCGAAATCTCATCAGGAAATAATTCGTGAGAA	449
QY	1605	agcaattagagaatactg 1623	
Db	450	AGACTTAAAGCTTAGACTG 468	

Search completed: September 6, 2002, 17:47:30
Job time: 9583 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 19:27:48 : Search time 5976.93 Seconds (without alignments) 5756.003 Million cell updates/sec

Title: US-09-581-241-5
Perfect score: 1644
Sequence: 1 atygaaacatgagaaacga.....agaaccagtgtgctaagatg 1644

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Searched:      1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%

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Database :

1:	genbmbl.*
2:	gb_ba.*
3:	gb_hgt.*
4:	gb_om.*
5:	gb_ov.*
6:	gb_pat.*
7:	gb_ph.*
8:	gb_pl.*
9:	gb_pr.*
10:	gb_ro.*
11:	gb_sts.*
12:	gb_sy.*
13:	gb_un.*
14:	gb_vl.*
15:	em_ba.*
16:	em_fun.*
17:	em_hum.*
18:	em_in.*
19:	em_mu.*
20:	em_om.*
21:	em_or.*
22:	em_ov.*
23:	em_pat.*
24:	em_ph.*
25:	em_pl.*
26:	em_ro.*
27:	em_sts.*
28:	em_un.*
29:	em_vl.*
30:	em_hgt_hum.*
31:	em_hgt_inv.*
32:	em_hgt_other.*
33:	em_hgtg_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description

1	1644	100.0	1644	6	E36480	Luciferase
2	1640.8	99.8	1644	6	E36479	Luciferase
3	1636	99.5	1644	6	AR098258	Sequence
4	1636	99.5	1644	6	E02495	CDNA encodl
5	1636	99.5	1644	6	E05448	CDNA sequen
6	1636	99.5	1644	6	E05448	CDNA sequen
7	1628.2	99.0	1908	3	LLUCI	l. lateralis
8	1628.2	99.0	1908	6	AR064317	Sequence
9	1628.2	99.0	1908	6	AR062709	Sequence
10	1628.2	99.0	1920	6	E16288	CDNA encodl
11	1620	98.5	2019	23	E10169	DNA encodin
12	1620	98.5	2055	23	E10170	DNA encodin
13	1619.6	98.5	1704	6	AR043316	Sequence
14	1619.6	98.5	1704	6	AR062708	Sequence
15	1619.6	98.5	1704	6	E12278	CDNA encodl
16	1619.6	98.5	1704	6	E13411	CDNA encodl
17	1618.4	98.4	2364	6	E13412	CDNA encodl
18	1357.6	82.6	1644	6	AR108849	Sequence
19	1357.6	82.6	1644	6	AR119318	Sequence
20	1357.6	82.6	1644	6	AR151719	Sequence
21	1357.6	82.6	1644	6	AX250561	Sequence
22	1357.6	82.6	1644	6	E01857	DNA encodin
23	1357.6	82.6	1644	6	E02267	DNA encodin
24	1357.6	82.6	1644	6	E03259	CDNA encodl
25	1357.6	82.6	1644	6	E05447	CDNA sequen
26	1357.6	82.6	1985	3	FEFLC	Luciola cru
27	1264.8	76.9	1656	6	AR098254	Sequence
28	1194.6	72.7	4573	3	LLU4182	Luciola lat
29	1188.2	72.3	2850	3	LLUCIFM2	l. lateralis
30	1187.8	72.3	4233	3	LLUCF5	l. lateralis
31	1187.8	72.3	4233	3	LLU49181	Luciola lat
32	1187.8	72.3	4233	3	LLU51019	Luciola lat
33	1042.4	63.4	1656	6	AR098253	Sequence
34	1042.4	63.4	1656	6	AR098255	Sequence
35	1016	61.8	1958	3	HOTLUCI	Sequence
36	1016	61.8	1970	23	E10030	Hotaria par
37	1014.4	61.7	2009	3	S61961	CDNA coding
38	817.2	49.7	1725	3	LNLDUCP	Luciferase
39	789.4	48.0	1647	3	AF328553	l. noctuilla
40	781.4	47.5	1922	3	PBILUCIF	Pyrococell
41	746.8	45.4	1773	3	PP91LNCNP	Pyrococell
42	746.8	45.4	1811	6	A37556	P. pyralis
43	746.8	45.4	4672	12	CVE277960	Sequence 22
44	746.8	45.4	4672	12	AX002437	Cloning v
45	746.8	45.4	5067	12	AF093665	Cloning vec
						Luciferase

ALIGNMENTS

RESULT	1
E36480	
LOCUS	1644 bp
DEFINITION	DNA linear PAT 07-FEB-2001
	Luciferase and method for assaying intracellular ATP by using the same.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 1644)	Notiaki H.S.M.M.	Luciferase and method for assaying intracellular ATP by using the	Patent: JP 199239493-A 07-SEP-1999;	OS Luciola lateralis PN JP 199239493-A/4 PD 07-SEP-1999 PF 21-DEC-1998 JP 1998363108 PR

FEATURES	
SOURCE	FH FT CDS Location/Qualifiers 1..1644 /organism="Luciola lateralis" /db_xref="taxon:7052"
BASE COUNT	529 a 262 c 348 g 505 t
ORIGIN	

Query Match	100.0%;	Score 1644;	DB 6;	Length 1644;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1644; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

QY	1	atggaaacaacatgaggaacgaatgaaanaaatggtgatggtcctgaacatttaccatt	60
Db	1	ATGGAACAACATGAGAACGATGAANAATATTGTGATGTGCTCGAACCATTTTACCCGATTT	60
QY	61	gaagaaggagatcgtctgtagaagcaaatctgcgcaagtaataatgatcgatatagtcaaaacttga	120
Db	61	GAAGAGGGGATCGTGTGAGAGCCAAATTCGCGAAGTATGTGATGTGATGTGCAAACTTGGCA	120
QY	121	gcaattgcttttactaacgcacctaaccgggtgctgattatacgtacggcggaataacttagaa	180
Db	121	GCAATTCGTTTTACTAACGCACCTTACCGGTGTGATTTATACGTACGCCGAATCTTAGAA	180
QY	181	aaatcatgctgctcctaagagaagqctttaaagaatatalgattggttgttgaatggaagaat	240
Db	181	AAATCATGCTGCTCTAGAGAGAGCGCTTTAAAGAAATATGTTGGTGTGTGATGAGAAAT	240
QY	241	gcgftatgacagtagaanaactgtagaagaattcttatactccgtatataagcggattattata	300
Db	241	GCGFTATGACAGTAGAANAACGTGGAAGAATCTTTATTCCTGTATTAGCGCGTTTATTATTATA	300
QY	301	gggtgcggtgtagcttccaacatagagatttacaactctacgtgaatggtgtccaaattta	360
Db	301	GGTGCGGGTGCGGTCCACACTAATGAGATTTAACCTCTACGTGATTTGGTTCACAGTTTA	360
QY	361	ggcatctctaaagccaacaattgtattagttcttaaaaaagaattagaataagttataact	420
Db	361	GGCATCTCTAAAGCCCAACAATTTGTTATTGTTCTTAAAAAGATTAGTAAAGTTTAAACT	420
QY	421	gtcaaaaaaacggtgaactgctatataaacaattgtatattgtgaacgaacgaatgagttct	480
Db	421	GTCAAAAAACCGTGAACCTGCTATTAAAAACAATTGTTATTATTTGACACGCCAAAGTGGATTTAT	480
QY	481	agaggtatcaatccatcagtagacaacttattataaaaaaacctccacaaggtttccaagaa	540
Db	481	AGAGGTTATCAATCCATGAGCAACTTATTAAAAAAAACCTCCACAGGTTTCMAAGGA	540
QY	541	tcaagttttaaactctgtagaagttaaacccgcaagaacaagttgctcttataatgaactct	600
Db	541	TCAAGTTTAAACCTGTGAGAGTTAAACCGCAAAAGMACMACTTCTCTTATTAAGAACTCT	600
QY	601	tcggggttcaacgggttgcgcaaaagtgctgcaacttaataaataatcgtcactaga	660
Db	601	TCGGGTTCAACCGGTTTGCCAAAAAGTGTCGAACCTTACTATGAANAATATCGTCACTAGA	660
QY	661	ttttctcaagcttagaataccaatttatagaaaccaagttccacaggaacaggtatattta	720
Db	661	TTTTCTCAAGCTTAGAGATCCAAATTATGGAACCAAGTTTCACCAAGGCAACGGTATTTTTA	720
QY	721	actgtagtagacaatccatcatatggttttgtaigttaacttaacttaagctatctactgt	780
Db	721	ACTGTAGTAGACATTCGATTCATGTGTTTGGTATGTTTACTACTTTAGGCTATCTMACTTGT	780
QY	781	ggatttgcgtatctgcacgttaaacgaatttgacgaagaagactttttaaacaactgcga	840
Db	781	GGATTTCGATTCGACGTTTACGAATTTGACGAAGAGACTTTTAAAAACACTGCGCA	840

QY	841	gaacaaatgctcaagcgttaactcttgaccagcttggctgaactcttaataagaat	900
Db	841	gatttcaaatatgttcaggcgttaattcttgaccagcttggctgaactcttaataagaat	900
QY	901	gaattactcgaataatgatgattatcacaatttagtctgaatgtcaatctgcggagaacct	960
Db	901	gaattactcgaataatgatgattatcacaatttagtctgaatgtcaatctgcggagaacct	960
QY	961	ttatctaaagaaatttggatgaagctgttctctagaagctttaaattaccgggtgttcgtcaa	1020
Db	961	ttatctaaagaaatttggatgaagctgttctctagaagctttaaattaccgggtgttcgtcaa	1020
QY	1021	ggcctatgtcttaacagaacaacccctcgaattatctacacccggaagcgatgataa	1080
Db	1021	ggcctatgtctttaaagcaaacacccctcgaattatctacacccggaagcgatgataa	1080
QY	1081	ccaagtgtctctcgcgaagaatttgcgtcatatttaaagcaaaagtatcgaatctgatact	1140
Db	1081	ccaagtgtctctcgcgaagaatttgcgtcatatttaaagcaaaagtatcgaatctgatact	1140
QY	1141	aaaaaaactttgggcccgcgaacgaagctggagaaatttggtaaaaggttcctatgtctatg	1200
Db	1141	aaaaaaactttgggcccgcgaacgaagctggagaaatttggtaaaaggttcctatgtctatg	1200
QY	1201	aaagtctatgataatcccaagaacaaacgaagaataatcatagatgaaagaagtttgatg	1260
Db	1201	aaagtctatgataatcccaagaacaaacgaagaataatcatagatgaaagaagtttgatg	1260
QY	1261	caacacaggaagatattggatlatcagaatgaagaanaaacattcttatcgttgatcgtttg	1320
Db	1261	caacacaggaagatattggatlatcagaatgaagaanaaacattcttatcgttgatcgtttg	1320
QY	1321	aagcttctaataacaaatacaaaagataataaagraccaactgcgtgaattgaactcttctt	1380
Db	1321	aagcttctaataacaaatacaaaagataataaagraccaactgcgtgaattgaactcttctt	1380
QY	1381	ttgcaacaatccaataatttttgatgacggcggttgcgttgagttccgaagatccctaatacgtgt	1440
Db	1381	ttgcaacaatccaataatttttgatgacggcggttgcgttgagttccgaagatccctaatacgtgt	1440
QY	1441	gaagctccggagagctgttctgtgatactaaagaagaataatctatagatcgtgaanaagaata	1500
Db	1441	gaagctccggagagctgttctgtgatactaaagaagaataatctatagatcgtgaanaagaata	1500
QY	1501	atggaattacgttgcagtcgaagttccaattcaaatgaagaagcttbgcgtggatgtccgtttt	1560
Db	1501	atggaattacgttgcagtcgaagttccaattcaaatgaagaagcttbgcgtggatgtccgtttt	1560
QY	1561	gtggaacgaagtaacctaaagatctcaactctgtaaaaatttgacgylaaagcaaatagagaata	1620
Db	1561	gtggaacgaagtaacctaaagatctcaactctgtaaaaatttgacgylaaagcaaatagagaata	1620
QY	1621	ctgaagaacacgaattgctaaagtg	1644
Db	1621	ctgaagaacacgaattgctaaagtg	1644

RESULT	2
E36479	
LOCUS	E36479 1644 bp DNA linear PAT 07-FEB-2001
DEFINITION	Luciferase and method for assaying intracellular ATP by using the same.
ACCESSION	E36479
VERSION	E36479.1 GI:13022686
KEYWORDS	JP 1999239493-A/3.
SOURCE	Luciola lateralis.
ORGANISM	Luciola lateralis. Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia; Cantharoidea; Lampyridae; Luciola.
REFERENCE	1 (bases 1 to 1644)
AUTHORS	Noriaki,H.S.M.M.
TITLE	Luciferase and method for assaying intracellular ATP by using the

Unclassified.
1 (bases 1 to 1644)
Hirokawa, K., Kajiyama, N. and Murakami, S.
TITLE Mutant-type bioluminescent protein, and process for producing the
mutant-type bioluminescent protein
JOURNAL Patent: US 6074859-A 13 13-JUN-2000;
FEATURES Location/Qualifiers
source 1..1644

BASE COUNT 528 a 260 c 350 g 506 t
ORIGIN

Query Match 99.5%; Score 1636; DB 6; Length 1644;
Best Local Similarity 99.7%; Pred. No. 0;

Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 atggaacacatggaagacgaataatctgtatgtatgtcttgaaccatttaccctatt 60
Db 1 ATGGAACACATGGAAGACGATGAAATATGTGTATGTCTGACCATTTACCCCTATT 60
QY 61 gaagagagatctgtctggaacacaaattgccaagtatatgtatgcatgatacttga 120
Db 61 GAAGAGGATCTGCTGGACACCAATTGCGCAATATATGATCGATATGCAAAACTTGA 120
QY 121 gaattgtcttactaacgcaactaccggtgtcgaattacgaacgcgaatacttaga 180
Db 121 GCAATTGCTTTACTAACCCACTTACCGGTGTGATATACGTACGCCCAATCTTAGA 180
QY 181 aaatcatgtcttctaggaagagccttaagaattatgttggttgttgaatga 240
Db 181 AAATCATGTCTGTAGAGAGCGCTTAAAGAAATATGTTGGTTGTATGAGAAAT 240
QY 241 ggcgtttagaagaaacgttgaagaattcttaccgttatgaacggtatttata 300
Db 241 GCGTTATGAGTAAGAAACGTGAGAAATCTTTATTCCTGTATTACCGGTTATTATA 300
QY 301 ggtctcggtgtgctcacaactaagatattacactcgaatgtgttcaagtta 360
Db 301 GGTGCGGTGTGCTCCAACTAATGAGATTATACCTCACTCAAGTATGTTGTCACAGTTTA 360
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Db 361 GGCATCTCTAAGCCAACTATGTATTAGTTCTAAAAAGAGATTAAAGTTATTAAC 420
QY 421 gtaacaaaacgtaactctatlaaacacatgttatatttgaacgcaaaagtgatt 480
Db 421 GTACAAAAACGGTAACCTCTATTAAACCATTTATATTTGACAGCAAGTGATTA 480
QY 481 agaggtatcaatccaatgacaacttatlaaaaaaacaactcacaagtttcaaga 540
Db 481 AGAGGTTATCAATCCATGACAACTTTATTAATAAAAAACAACCTCCACAGGTTTCAAGGA 540
QY 541 tcaagttttaaactgttagaagttlaacgcgaagaacagttgtcttataatgaact 600
Db 541 TCAAGTTTAAACTGTAGAGTTAAACCCCAAGAACAGTTGCTCTTATATGAACCTCT 600
QY 601 tcgggttcaacgggtttgcacaaagtgtaacacttaccatgaataatcgtcactaga 660
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QY 781 ggttttcgattgtcatgttaacgaaatttgacgaagaacatttttaaaacacgcaa 840
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QY 841 gattacaatgttcaagcgttactctgtacacgaacttgttgaacttcttaataaga 900
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QY 901 gaattcctgataaataatgattatcaaatlttagttgaaattgcatcgtgaggaacct 960
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Db 1141 AAAAAACCTTTGGCCCGACAGACAGCTGGAGAGTTTGTCTAAAGGCTCTATGCTTATG 1200
QY 1201 aaagttatgataataatccaagaacaagaagaatacatagaagaagttgtgtg 1260
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QY 1501 atggaatcgttctgaatgaagttcaaatgcaaaacgttgcgtgtgtgtcgtttt 1560
Db 1501 ATGGAATTACGTTCTGATCAAGTTCAAAATGCAAAACGTTTGGCTGTGTGTCGCTTT 1560
QY 1561 gtgacgaagttacctaaggttctcaactgttaaaatltgaacggtlaaagcaattaga 1620
Db 1561 GTGACGAAGTACCTTAAGGCTCTCACTGTGTAATAATTGACGCTAAACCAATTAGAAATTA 1620
QY 1621 ctgaagaagaacagttgtctaagatg 1644
Db 1621 CTGAAGAAGCAAGTGTCTTAAGATG 1644

RESULT 4
E02495 LOCUS E02495 1644 bp RNA linear PAT 29-SEP-1997
DEFINITION E02495 cDNA encoding luciferase.
ACCESSION E02495.1 GI:2170725
VERSION JP 1990171189-A/1.
KEYWORDS Luciola lateralis.
SOURCE Luciola lateralis.
ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia; Cantharoidea; Lampyridae; Luciola.

REFERENCE
AUTHORS Kajiyama, N., Tatsumi, H. and Nakano, E. .
TITLE LUCIFERASE GENE
JOURNAL Patent: JP 1990171189-A 1 02-JUL-1990;

COMMENT

KIKKOMAN CORP
OS Luciola lateralis
PN JP 1990171189-A/1
PD 02-JUL-1998
PF 22-DEC-1988 JP 1988322029
PI KAIJIYAMA NAOKI, TATSUMI HIROKI, NAKANO EIICHI PC
C12N15/53//C12N9/02;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FT mat_peptide 1..1644
/product='Luciferase'.
/organism='Luciola lateralis'
/db_xref='taxon:7052'

FEATURES

source
1..1644
Location/Qualifiers

BASE COUNT 529 a 262 c 349 g 504 t
ORIGIN

Query Match 99.5%; Score 1636; DB 6; Length 1644;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 61 GAAGAGGATCTGCTGAGACCATTCGCAAGATATATGATGCATATGCAAACTTGGGA 120
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QY 841 gattacaatgttcaaggttattctctgtacagacttgtttgcaattcttaagaagt 900
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QY 901 gaattactgataaataatattatcaaatgaattgaattgcaatctgcggaacact 960
DB 901 GAAATTCGTCAATTAATATGATTTATCAAAATTTAGTTGAATTTGCATCTGCGGACACT 960
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DB 1141 AAAAAAATTTGGCCCGCAACAGACGTGAGAGTTTGTGTTAAAGGCTCTATGCTTATG 1200
QY 1201 aaaggtatgtatagataatccagaagcaacaagaagaatacagatgaagaaggttgtg 1260
DB 1201 AAAGGTATCTAGATATATCCGAAGCAACAGAAATCATATGATGAAAGAGTTGGTGG 1260
QY 1261 cacacagagaatatttgatatacgaatgaagaanaacatttcttactgtgtgacgttg 1320
DB 1261 CACACAGAGATATTGGGATTTAGATGAGAAACAAATTTCTTATCTGTGATCGTTTG 1320
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DB 1321 AAGCTTTTATCAATAACAAAGATATCAAGTACCAACGCTGCAATTAGAATCTGTTCT 1380
QY 1381 ttgcaacatccaaatatttttgaatccggcgtgtgtcgtgtccagatccatagctgtg 1440
DB 1381 TTGCAACATCCAAATATTTTTGTATGCGCGGCTTGTGCGGTTCAGATCTTATAGCTGCT 1440
QY 1441 gacgttccgggaagctgtgtgttacttaagaagaagaatactatgaactgaagaaga 1500
DB 1441 GACGTTCCGGGAGCTGTGTGTACTTGAAGAAAGAAATCTATGACTGAAAAAGAAAGTA 1500
QY 1501 atggaatcagttgtcagtlcaagtlccaatgcaaaaacglttgcgtgtgtgtt 1560
DB 1501 ATGGAATCAGTTCCTGCTAGTCAAGTTTCAAAATGCAAAACGTTGCTGTGTGTGCTT 1560
QY 1561 gtggaagaagttaccataaaggttccactgtgtaaaaatgtgaaggttaagaagaata 1620
DB 1561 GTGGAAGAAAGTTACCTAAAGGCTTCACGTGTAATAATTGACGCTAAACCAATTAGAGAAATA 1620
QY 1621 ctgaagaacacagttgtcgaatg 1644
DB 1621 CTGAAGAACCAAGTTGCTTAAGATG 1644

RESULT 5
LOCUS E05448 1644 bp RNA linear PAT 29-SEP-1997
DEFINITION CDNA sequence of Luciferase.
ACCESSION E05448
VERSION E05448.1 GI:2173637

Db 1561 GTGACGACGAGTACTAAAGGCTCTACCTGGTAAATTTGACGGTAAAGCAATTAGAGAAATA 1620

QY 1621 ctgaagaaacagatctgctaagatg 1644
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Db 1621 CTGAAGAAACAGTGTCTAAGATG 1644

RESULT 6

LLUCI 1781 bp mRNA linear INV 24-NOV-1993

LOCUS L. lateralis luciferase mRNA.

DEFINITION X66919.1 S38389

ACCESSION X66919.1 GI:9526

VERSION luciferase.

KEYWORDS Japanese firefly.

SOURCE Eukarya: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta: Phryganea: Neoptera: Endopterygota: Coleoptera: Polyphaga: Elateriformia: Cantharoidae; Lampyridae; Luciola.

REFERENCE 1 (bases 1 to 1781)
Tatsumi, H., Kajiyama, N. and Nakano, E.
Molecular cloning and expression in *Escherichia coli* of a cDNA clone encoding luciferase of a firefly, *Luciola lateralis*

JOURNAL Biochim. Biophys. Acta 1131 (2), 161-165 (1992)

REFERENCE 2 (bases 1 to 1781)
Tatsumi, H.
Direct Submission
Submitted (21-JUL-1992) H. Tatsumi, Research and Development Division, Kikkoman Corporation, 399 Noda, Noda City, Chiba 278, JAPAN

FEATURES

source location/Qualifiers

1..1781
/organism="Luciola lateralis"
/db_xref="taxon:7052"
59..1705
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BASE COUNT 579 a 276 c 367 g 559 t

ORIGIN

Query Match 99.5%; Score 1636; DB 3; Length 1781;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 239 AAATCATGCTGCTAGAGAGCGCTTTAAAGATTATGCTTTGTTGTATGAGAAAT 298

QY 241 ggcgtatgcagtgaaacacgctgtaagatcttattccctgtaagccggtattata 300
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Db 299 GCGTTATGCAGTGAANAACGTGTAGAGATCTTTATTCTGTAATTACCGGTTATTATA 358

QY 301 ggtgctgctggtgctcaactaatgagattcaactctacgtgaattggtccagttta 360
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Db 359 GGTGTCGTGTGCTGCCACACTAATGAGATTTACACTACAGGAAATGGTCCACAGTTTA 418

QY 361 ggcactctcaagccaaactatgattgattcttaaaaaagattagataaattact 420
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Db 419 GGCATCTCTAACCCAACTATGTATTACTTAAAGATTAAGTTAAAGTTAAACT 478

QY 421 gtcaaaaaacggtiaactctttaaaccattgattatgtgaacgcaagtgtgatt 480
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Db 479 GTACAAAACCGTACTCTATTAAACCATTTGTTATTTGACAGCAAGGGATTTAT 538

QY 481 agaggtatcaatccatgacacacttataaaaaaacactccacaaagttccaagga 540
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Db 539 ACAGGTTATCATTCATGACACAACTTTATTAATAAAACACATCCACAAAGTTTCAAGA 598

QY 541 tcaagttttaaaccctgtagaagtttaacgcgaagaacaaagttgctcttataatga 600
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Db 599 TCAGTTTAAACCTGTAGAGTTAACCCCAAGAAAGAAAGTTGCTTTATATGAACCTCT 658

QY 601 tctggttcaacccggtttgccaagaagtgctgaactaccatgaaatctgcactaga 660
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Db 659 TCGGGTTCAACGGGTTTGCANAAGGTGTGCAACCTTACTCATGANAATCCAGCTACTAGA 718

QY 661 tttctcaacgctagagatccaattatagaaacaaagttccacgaagccagctattta 720
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Db 719 TTTTTCACAGCTAGAGATCCAAFTTATGGAACCAAGTTTCAACAGCAGCGGTATTTA 778

QY 721 actgtagtaacatccatcaatgagtttgatgattactactttaggtactactgct 780
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Db 779 ACTGTAGTACCATTCATCATCATGTTGGTATGTTACTTACCTTACCTATCACTGT 838

QY 781 gctttcgtatgctcatgcttaacgaatttgacgaagaaactttttaaaccacgca 840
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Db 839 GGTTCGTATGTCATGTTAAAGAAATTTGACGAAGAACCTTTTAAACACCTGCA 898

QY 841 gattcaaaatgctcaagccttattctgtgacgaactttgtgcaattcttaataaagt 900
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Db 899 GATTCAAAATGTTCAAGCTTATTTCTGTACGACATTTTGTGCATTTTATATNAACT 958

QY 901 gaattactcgataaataatgattatcaaaattagttgaattgcatctgagcgagcact 960
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Db 959 GAATTACTCGATTAATATGATTATCAAAATTTAGTTGAATTTGCAATTCGCGAGCACCT 1018

QY 961 ttatctaaagaatgtgtaagcgtgtgtgaacgttttaattaccgggtgttctgcaa 1020
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Db 1019 TTATCTAAAGAAATGTGTAAAGCTGTGCTAGACGTTTAAATTTACGGGTTGCTCA 1078

QY 1021 ggcatagtgtttaaagaaacacactctgcaattatatacacacggaagcgatgataa 1080
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QY 1141 aaaaaaacttggtgcccgaacagaagtggaagaatttggttaaaggtctctgcttag 1200
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Db 1199 AAAAAAATCTTGGCCCGAACAGAGCTGGAGAAATTTGTTAAAGGCTCTATGCTTAG 1258

QY 1201 aaaggtatgataatccagaacaaagaagaatcatatagatgaagaagttgctg 1260
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Db 1259 AAAGGTATGATGATTAATCAGACGACAAAGAAATATATGATGAAGAAGTTGCTTG 1318

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Db 1319 CACACAGAGATATTGGTATTACGATGAAGAAACATTTCTTATCGTGATCGTTTG 1378

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Db 1619 GTGAGAGAGTACCTAAGGTCTCAGTGGTAAATTAAGAGTAAGCAATTAGAGAAATA 1678
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RESULT 7

AR043317

LOCUS AR043317 1908 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 8 from patent US 5814465.
ACCESSION AR043317
VERSION AR043317.1 GI:5964325

KEYWORDS

SOURCE .
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1908)

AUTHORS Tatsumi,H., Fukuda,S., Kikuchi,M. and Koyama,Y.
TITLE Biotinlated firefly luciferase, a gene for biotinlated firefly

luciferase, a recombinant DNA, a process for producing biotinlated
luciferase and a bioluminescent analysis method
Patent: US 5814465-A 8 29-SEP-1998;

FEATURES
Location/Qualifiers
1..1908

SOURCE

/organism="Unknown"

BASE COUNT 598 a 329 c 426 g 555 t

ORIGIN

Query Match

Best Local Similarity 99.0%; Score 1628.2; DB 6; Length 1908;

Matches 1633; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 atggaacaatggaagaacgtgaataatctgtatgtgtcctgaacatttaacctatc 60
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QY 61 gaagagggatctgctgagacacattgccaagtatalagatcgatatgaagaattgga 120
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QY 121 gcaatgcttllaactaacgacttaacgctgtgcatatatacgtacgccaataactagaa 180
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Db 121 GCATTTGCTTTACTAACGACACTTACCGGTGCTGATTATACGTAACCGCAATCTTAGAA 180
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QY 181 aaatcatgctgtctagagagagctttaaagaatctatgtgtgttgaatgaagaatt 240
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Db 181 AAATCATGCTGTCTAGAGAGGCTTTAAAGAAATATGTTGTTGTTGATGGAAGAAAT 240
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QY 241 gggtttaaggaagaacgctgaagaattcttattccgttatagccggttattata 300
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Db 1501 ATGATTACGTTGTGTACTTCAAGTTTCAATGCAAAACGTTTGGCTGTGTGCTGCTTTT 1560
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QY 1621 ctgaagaacaagctgtgtaag 1641
Db 1621 CTGAAGAAACCGTTGCTAAG 1641

RESULT 8
AR062709
LOCUS AR062709 1908 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 8 from patent US 5843746.
ACCESSION AR062709
VERSION AR062709.1 GI:5990400
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1908)
AUTHORS Tatsumi,H., Fukuda,S., Kikuchi,M. and Koyama,Y.
TITLE Biotinlated firefly luciferase, a gene for biotinated firefly luciferase, a recombinant DNA, a process for producing biotinated luciferase and a bioluminescent analysis method
JOURNAL Patent: US 5843746-A 8 01-Dec-1998;
FEATURES
source 1..1908
Location/Qualifiers
BASE COUNT 598 a 329 c 426 g 555 t
ORIGIN

Query Match 99.0%; Score 1628.2; DB 6; Length 1908;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1633; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 361 GGCATCTTAAGCCAACTATGTTAGTCTAAAAAGATAGATTAAGTATTAAC 420
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Db 421 GTACAAAAACGTAACCTCTATTAACCATTTGTATTTGGACAGCAATGATATAT 480
QY 481 agagttatcaatccatggaacacttataaaaaaacatccacaaagtttcaaaaga 540
Db 481 AGAGTTATCAATCCATGAGCAACCTTTATTAATAAAAAACATCCCAAGGTTTCAAGGA 540
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QY 1141 aaaaaaacttggcccgcaagaacgltgagaagttltgtlaaagggttcttactgtatg 1200
Db 1141 AAAAAAATTTGGCCCGCAACACGCTGGAGAGTTGTGTAAGGCTCTATGCTTATG 1200
QY 1201 aaagtltatgataataccagaagaacaagaagaatacatagatlaagaaggttgtgtg 1260
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QY 1261 cacacagagatatgtggtatctagatgaagaanaaacatttcttactgtgtatgtgtg 1320
Db 1261 CACACAGAGATATTTGGTATGATGAGTGAAGAAAAACATTTCTTATTCCTGATCGTTTG 1320
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QY 1621 ctgaagaacacagttgctaa 1641
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DB 1621 CTGAGAGAAACCACTTGTCTAAG 1641

RESULT 9
E12279 1908 bp DNA linear PAT 24-JUN-1998
LOCUS E12279
DEFINITION CDNA encoding biotinylated Luciola luciferase.
ACCESSION E12279
VERSION E12279.1 GI:3251113
KEYWORDS JP 1996308578-A/4.
SOURCE Luciola lateralis.
ORGANISM Luciola lateralis
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Elateriformia; Cantharoidea; Lampyridae; Luciola.
1 (bases 1 to 1908)
Tatsumi, H., Fukuda, M., Kikuchi, M. and Koyama, T.
BIOTIN FIRE FLY LUCIFERASE. BIOTIN FIRE FLY LUCIFERASE GENE, NEW
RECOMBINANT DNA, PRODUCTION OF BIOTIN FIRE FLY LUCIFERASE AND
BIOLUMINESCENCE ANALYSIS
Patent: JP 1996308578-A 4 26-NOV-1996;
KIKKOMAN CORP
COMMENT OS Luciola lateralis
PN JP 1996308578-A/4
PD 26-NOV-1996
PF 24-APR-1995 JP 1995098857
PR 27-JUL-1994 JP 94P 193798, 14-MAR-1995 JP 95P 54625 PT
TATSUMI HIROKI, FUKUDA MASARU, KIKUCHI NAMORU, KOYAMA TAJUJI PC
C12N15/09, C12N9/02, C12Q1/26, (C12N9/02, C12R1:185); CC
strandedness: Double;
CC topology: Unknown;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FH source 1..1908
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FT mat_peptide 1..1908
FT Location/Qualifiers
FT 1..1908
/db_xref='taxon:7052'
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FEATURES
source
BASE COUNT 598 a 329 c 426 g 555 t
ORIGIN

Query Match 99.0%; Score 1628.2; DB 6; Length 1908;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1633; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 atggaacaatggaagaacatgaataatgtgtatgctcgaacatttaccatt 60
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DB 61 GAAGAAGGATCGTCTGGAACAAATGCTGAAGATLATGCATCGAATATCAAAACTTGA 120
QY 121 gcaattgcttactaagcactaccggtgctgattatagtaacgcgaacttagaa 180
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DB 121 GCAATTTGCTTTTACTAACGCACTTACCGGTGTCGATTATACGTACGCCGGAATCTTAGAA 180
QY 181 aaatcatgctgctttagagaagccttaagaatattagttgtgttgaagaatt 240
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DB 181 AAATCATGCTGCTTAGAGAGGCTTTAAAGAAATTAAGTTTGGTTGTGTGAGAGATT 240
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DB 301 GGTGTGCGTGTGTGCTCCAACTTAATGAGATTATACCTCTACGTAATTTGGTTCACAGTTTA 360
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DB 361 GGCATTCTCTAAGCCAACTTGTATTAGTTCTTAAAAAGAGATTAAATTAAGTTATTAACT 420
QY 421 gtacaaaaaacggttaactgtctatlaaaaccattgttataatgacagcaagtgtat 480
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DB 421 GTACAAAAAACGGTAACTGCTATTAAACCATTTGTTATTTGACAGCAAGTGATTTAT 480
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DB 601 TCGGTTCAACGGTTTGCCAAAAGGTGACACTTACCATGAAATTTGGTCACGCGT 660
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DB 661 TTTTCTCACGCTAGAGATCCAAATTTATGAAACAAAGTTTACCAAGGCGCTATTATTA 720
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DB 721 ACTGTATGACATTCATCATGATGTTTGGTATGTTTACACTTAAAGCTATCTAACTTGT 780
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QY 841 gatlaaataatgtaacagcgttattctgtacagactgtttgcaatttotaatagaagt 900
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DB 841 GATTACAAATGTTCAAGCGTTATCTTGTACCGCACTTTGTTCCAATTTTAAATGAGAAGT 900
QY 901 gaattactgataaataatgatattatcaaatatgaattgaattgcattgctgcgaagcct 960
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QY 961 ttatctaaagaatgtgtgaagcgtgtgtgtagacgttttaattacgggtgtgtgca 1020
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LOCUS	El6288	1920 bp	DNA linear PAT 28-JUL-1999
DEFINITION	DNA encoding fusion protein which comprises luciferase and lysostaphin.		
ACCESSION	El6288		
VERSION	El6288.1	GI:5710971	
KEYWORDS	JP 1998150991-A/1.		
SOURCE	unidentified.		
ORGANISM	unidentified.		
REFERENCE	1 (bases 1 to 1920)		
AUTHORS	Tatsumi,H., Fukuda,M. and Nagahara,A.		
TITLE	LUCIFERASE-LYOSTAPHRIN FUSED PROTEIN, ITS PRODUCTION AND BIOLOGICAL ANALYSIS USING THE SAME		
JOURNAL	Patent: JP 1998150991-A 1 09-JUN-1998; KIKKOMAN CORP		
COMMENT	OS None		
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	PN JP 1998150991-A/1		
	PD 09-JUN-1998		
	PF 25-NOV-1996	JP 1996328042	
	PI TATSUMI HIROKI, FUKUDA MASARU, NAGAHARA AYUMI	PC	
	CI1915/09,C07H21/04,C07K19/00,C12N9/02,C12N9/52,C12P21/02, PC		
	CI201/66,		
	PC (C12N9/02,C12R1:19),(C12N9/52,C12R1:19);		
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	CC topology: Linear;		
	CC hypothetical: No;		
	CC anti-sense: No;		
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AC E10169;
XX E10169;
SV E10169.1
XX 08-OCR-1997 (Rel. 52, Created)
DT 02-SEP-2000 (Rel. 65, Last updated, Version 2)
XX DNA encoding streptavidin-firefly luciferase fusion protein.
DE JP 1995289264-A/1.
XX unclassified.
OS unclassified.
XX unclassified.
RN [1]
RP 1-2019
RA Tatsumi H., Fukuda M.;
RT "VARIANT TYPE STREPTAVIDIN GENE, FUSION PROTEIN GENE OF VARIANT TYPE
RT STREPTAVIDIN-FIREFLY LUCIFERASE, NEW RECOMBINANT AND PRODUCTION OF FUSION
RT PROTEIN OF VARIANT TYPE STREPTAVIDIN-FIREFLY LUCIFERASE";
RL Patent number JP1995289264-A/1, 07-NOV-1995.
RL KIKKOMAN CORP.
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XX OS None
XX OC Artificial sequences.
XX PN JP 1995289264-A/1

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CC PD 07-NOV-1995
CC PF 27-APR-1994 JP 1994090275
CC PI TATSUMI HIROKI, FUKUDA MASARU
CC PC C12N15/09,C07K14/36,C07K19/00,C12P21/02,G01N33/53,(C12P21/02,
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CC CC anti-sense: No;
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CC FH source 1..2019
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Query Match 98.5%; Score 1620; DB 23; Length 2019;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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DEFINITION Sequence 5 from patent US 5843746.
ACCESSION AR062708
VERSION AR062708.1 GI:5990399
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1704)
AUTHORS Tatsumi,H., Fukuda,S., Kikuchi,M. and Koyama,Y.
TITLE Biotinized firefly luciferase, a gene for biotinated firefly luciferase, a recombinant DNA, a process for producing biotinated luciferase, and a bioluminescent analysis method
JOURNAL Patent: US 5843746-A 5 01-DEC-1996;
FEATURES
source Location/Qualifiers
BASE COUNT 541 a 275 c 361 g 527 t
ORIGIN

Query Match 98.5%; Score 1619.6; DB 6; Length 1704;
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Matches 1625; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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OY 1511 ttgctagtcgaagttlcaaalgcacaaacglttcgtgtgtgtgtccgttctgtgacgaag 1570
 DB 1571 TTGCTAGTCAAGTTTCAANTGCAAAACGTTTGGCTGTGTGTGTCGTTTGTGTGAGGAAG 1630
 OY 1571 taccataaggtctcactgtgtaaaattgacggttaagaacaaactagaataactgaagaac 1630
 DB 1631 TACCTAAAGTCTCACTGGTAAATTTGACGATTAACCAATTTAGAGAAATACGAAGAAC 1690
 OY 1631 caattgtaagaatg 1644
 DB 1691 CAGTTCCTAAGATG 1704

RESULT 15
 E12278
 LOCUS E12278 1704 bp DNA linear PAT 24-JUN-1998
 DEFINITION CDNA encoding biotinylated Luciola luciferase.
 ACCESSION E12278
 VERSION E12278.1 GI:3251112
 KEYWORDS JP 1996308578-A/3.
 SOURCE
 ORGANISM
 Luciola lateralis
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 Elateriformia; Cantharoidae; Lampyridae; Luciola.

REFERENCE
 AUTHORS Tatsumi,H., Fukuda,M., Kikuchi,M. and Koyama,T.
 TITLE 1 (bases 1 to 1704)
 BIORN FIRE FLY LUCIFERASE, BIOTIN FIRE FLY LUCIFERASE GENE, NEW
 RECOMBINANT DNA, PRODUCTION OF BIOTIN FIRE FLY LUCIFERASE AND
 BIOLUMINESCENCE ANALYSIS
 Patent: JP 1996308578-A 3 26-NOV-1996;
 KIKKOMAN CORP

JOURNAL
 COMMENT
 OS Luciola lateralis
 PN JP 1996308578-A/3
 PD 26-NOV-1996
 PF 24-APR-1995 JP 1995098857
 PR 27-JUL-1994 JP 94P 193798, 14-MAR-1995 JP 95P 54625 PI
 TATSUMI HIROKI, FUKUDA MASARU, KIKUCHI MAMORU, KOYAMA TAJUJI PC
 C12N15/09,C12N9/02,C12Q1/26,(C12N9/02,C12R1:185); CC
 strandedness: Double;
 CC topology: Unknown;
 CC hypothetical: No;
 CC anti-sense: No; Location/Qualifiers

FEATURES
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 FT /clone='pHLF203' /product='biotinylated Luciola luciferase'.
 FT mat_peptide 1..1704
 FT Location/Qualifiers
 1..1704
 /organism='Luciola lateralis'
 /db_xref='taxon:7052' 527 t

BASE COUNT

541 a 275 c 361 g 527 t

ORIGIN

Query Match 98.5%; Score 1619.6; DB 6; Length 1704;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1625; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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 DB 131 CTGCTGGAGACCAATTTGCCCAAGTATATGATCATGATATGCAAAACTTGGAGCAATTGCTT 190
 OY 131 ttactaagcacttaccggtgtcgtatctatagctacgcgaatcttaagaataatcgtct 190
 DB 191 TTACTTACGCACTTACCGGTGTGATTTATGCTAGCGCGAATTAATTAGAAAAATCATGCT 250

QY 191 gctcagaagagccttaagaatlatggttggcttgatggaagaatgctatgca 250
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Db 251 GTCTAGAGAGGCTTTAAAGATATATGTTGGTTGATGAGGAAGATTCGCTTATGCA 310
QY 251 gtaaaacgtggaagaatccttattcccgatatagcggttatttataagtgctggt 310
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Db 311 GTGAAACTGTGAAGAGCTTTTATCTCTGATATAGCGGCTTATTTATAGTGTGCGGTG 370
QY 311 tggctcaactaatgaattacaccttaagctgaattggttcaagaatttaggactccta 370
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Db 371 TGGCTCCAACTAATGAAATTTACCTGACGTGAATGGTTGCACAGTTTAAAGCATCTCTA 430
QY 371 agccaacaattgtattagttcttaaaaaagattagaataagctataacttacaaaaaa 430
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Db 431 AGCCAAACAATTTGATTTAGTTCTFAAAAAAGATTAGATTAAGTTATACCTTACAAAAA 490
QY 431 cggtaactgctatnaaaccattgtataltggaagcaaaagtgaattatagaagttatc 490
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Db 491 CGGTAACTGCTATTTAAACCATGCTTTATTTGACACCAAAAGTGAGTTATAGAGTTATC 550
QY 491 aatccatggaacatttatttaaaaaaacctccacaaggttcaaaagatcaagtttta 550
|||||
Db 551 AATCCATGAGCAACTTATTTAAAAAAAACCTCCACAAGTTTCAAGGATCAAGTTTAA 610
QY 551 aaactgagaagtttaacgcaaaagaacaagttgctcttataatgaactctcggttcaa 610
|||||
Db 611 AAACGTGAGAGTTAAACCGCAAAAGACAGTGTCTTATATATCAACTCTTGGGTTTCA 670
QY 611 ccggttgcgaanaagtgtaacacttaacatgaanaaalcgtaactagatttctcaag 670
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Db 671 CCGGTTTGCCAAAAAGGTGTGCAACTTACTCATGAAATTTGTGTCACGGTTTCTCAGC 730
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Db 791 CATTCGATCATGTTTGGTATGTTTACTACTTATAGGCTATCTACTTGTGTGTTTCGTA 850
QY 791 ttgtcatgtttaacgnaatttgaacgaagaagacttcttaaaaaacatgcaagattacaat 850
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Db 851 TTGTCAATGTTAAGCAAAATTTGACGAGAGAGACTTTTAAAAACACTGCAAGATTACAAAT 910
QY 851 gttcaagcgttattctgtaccgaacttggttggcaattcttaataagaagtgaattactcg 910
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Db 911 GTTCAAGCGTTATTTCTGTACCGACTTGTGCAATTTTAAATGAAAGTGAATTACTCG 970
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QY 1031 taacagaanaaacctctgcgaattatatacaaccggaagcgatgataaaccagtgctt 1090
|||||
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QY 1091 ctggcaagttgtgcaattttaaagcaaaagttatcgatctgataacttaaaaaaactt 1150
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Db 1151 CTGGCAAAAGTTGTGCCATTTATTTAAAGCAAAAGTTATCGATCTTGATATCTAAAAAACTT 1210
QY 1151 ttgggccgaacagacgttgaagaagttgtgtlaaagggtlccatgctatagaagaagttatg 1210
|||||
Db 1211 TGGGCCCGAAGACAGACGTGGAAGAGTTGTGAAGGCTCTATGCTTATGAAGGTTATG 1270
QY 1211 taagtaatccaagaagcaagaagaaatcctaagttgaagaaggttggttgcaacagagag 1270
|||||
Db 1271 TAGATATTCAGAAAGCAAGAGAAATCATAGATGAAGAGGTTGTTCACACAGAGAG 1330

QY 1271 atattgglatlacatgaagaanaaacaattcttattatcgatgatcggttgaagctcttaa 1330
|||||
Db 1331 ATATTGGTATTACATGAAGAAAAACATTTCTTATGTGTGATGCTTGAAGTCTTTAA 1390
QY 1331 tcaatlaaagaagatalcaagtlaccacactgctgaattagaatcgttcttcttgaacatc 1390
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Db 1391 TCAATATCAAAAGATATCAAGTACACCTGCTGAATTTGAATCTGTCTTTTGCAACATC 1450
QY 1391 caaatattttgtagcgcggttgctgagcttccagatccatagatcgttgagctccgg 1450
|||||
Db 1451 CAAATATTTTGTGATGCCGCGGTGCTGGCTTCCAGATCTATATGCTGTAGACTTCCGG 1510
QY 1451 gacgtgttctgtactlaagaagaanaaactatgaactgaaanaaagtaatgaatgaacg 1510
|||||
Db 1511 GAGCTGTTGTTGTACTTGAAGAAATCTATGACTGAGAAAGAAATGATATGATTAAG 1570
QY 1511 ttgttagtcaagtttcaaatgcaaaagtttgctggtgtgtgctcgttltgtggaagag 1570
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Db 1571 TTGCTAGTCAAGTTTCAAAATGCAAAACGTTTGCAGTGTGTGCTCCGTTTGTGAGCAGAG 1630
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Db 1631 TACCTAAAGGTCTCACTGTAAATTTGACGGTAAAGCAATTTAGAGAAATGACTGAAGAAAC 1690
QY 1631 caattgctaaagtg 1644
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Db 1691 CAGTTGCTAAGATG 1704

Search completed: September 6, 2002, 19:28:23
Job time: 15466 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 19:38:41 : Search time 512.01 Seconds
(without alignments)
5512.797 Million cell updates/sec

Title: US-09-581-241-5
Perfect score: 1644
Sequence: 1 atggaacaatcgtggaacga.....agaacacgtgtcgaatg 1644

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1644	100.0	1644	20	AAx84396
2	1640.8	99.8	1644	20	AAx84395
3	1636	99.5	1644	14	AAQ34745
4	1636	99.5	1644	20	AAx25718
5	1632.8	99.3	1644	11	AAQ03257
6	1628.2	99.0	1908	18	AAr63369
7	1628.2	99.0	1920	19	AAV32467
8	1620	98.5	2019	17	AAr33850
9	1620	98.5	2055	17	AAr33851

10	1619.6	98.5	1704	18	AAr63268	Firefly Luciferase
11	1619.6	98.5	1704	19	AAV23595	Antibody-Firefly 1
12	1618.4	98.4	2364	19	AAV23580	Antibody-Firefly 1
13	1490.4	90.7	1656	20	AAx25717	Firefly Luciferase
14	1357.6	82.6	1644	10	AAr91170	Recombinant lucifer
15	1357.6	82.6	1644	11	AAQ03801	Recombinant lucifer
16	1357.6	82.6	1644	12	AAQ13844	Luciferase mutant
17	1357.6	82.6	1644	22	AAQ92231	Modified luciola c
18	1357.6	82.6	1644	24	AAQ22186	Luciola cruciata 1
19	1356	82.5	1644	12	AAQ13825	Luciferase. Lucio
20	1356	82.5	1644	14	AAQ34987	Thermotable lucif
21	1354.4	82.4	1644	12	AAQ13840	Luciferase mutant
22	1354.4	82.4	1644	12	AAQ13841	Luciferase mutant
23	1354.4	82.4	1644	12	AAQ13842	Luciferase mutant
24	1354.4	82.4	1644	12	AAQ13843	Luciferase mutant
25	1354.4	82.4	1644	12	AAQ13845	Luciferase mutant
26	1264.8	76.9	1656	20	AAx25716	Firefly Luciferase
27	1042.4	63.4	1656	20	AAx25715	Firefly Luciferase
28	1016	61.8	1970	16	AAr00613	DNA encoding lucif
29	750	45.6	10533	16	AAQ98930	Vector p39neoluc s
30	750	45.6	10558	16	AAQ98912	TGF-beta responsiv
31	749.6	45.6	6565	22	AAr55126	Nucleotide sequenc
32	749.6	45.6	6971	22	AAr55124	Nucleotide sequenc
33	749.6	45.6	7958	22	AAr55125	Nucleotide sequenc
34	749.6	45.6	7969	22	AAr55123	Nucleotide sequenc
35	747.4	45.5	5427	22	AAr83390	Luciferase reporte
36	746.8	45.4	1811	15	AAQ58732	Encodes firefly lu
37	746.8	45.4	5620	18	AAr48630	Ad5-ITR. CMV-Lucif
38	746.8	45.4	5620	22	AAr30233	Minimal adenovirus
39	746.8	45.4	5789	20	AAx08779	pgL2-Promoter gene
40	746.8	45.4	5791	20	AAx08778	pgL2(GST-ARE)SV40/
41	746.8	45.4	5793	20	AAx08776	pgL2(lapo AI-ARE)SV
42	746.8	45.4	5793	21	AAx08777	pgL2(lapo AI-mARE)S
43	746.8	45.4	5818	20	AAx38352	Plasmid pGL2 (lapo
44	746.8	45.4	5819	21	AAx08775	pgL2(lapo AI-49t mu
45	746.8	45.4	5819	20	AAx08774	pgL2(lapo AI-250)lu

ALIGNMENTS

RESULT 1	AAx84396	standard; DNA; 1644 BP.
ID	AAx84396;	
XX	AAx84396;	
AC	09-SEP-1999	(first entry)
DT		
XX		
DE	L. lateralis	Luciferase coding sequence.
XX		
KW	Luciferase; surfactant-tolerant; firefly; intracellular ATP assay; ss.	
OS	Luciola lateralis.	
XX		
PN	WO9933997-A1.	
XX		
PD	08-JUL-1999.	
XX		
PF	24-DEC-1998;	98WO-JP05864.
XX		
PR	26-DEC-1997;	97JP-0361022.
XX		
PA	(KIKK) KIKKOMAN CORP.	
XX		
PI	Hattori N, Murakami S;	
XX		
DR	WPI: 1999-419109/35.	
XX	P-PSDB; AAV22183.	
PT	Modified luciferase tolerant to surfactants and useful for assay of	
XX	Intracellular ATP	

OS Luciola lateralis.
XX MO9933997-A1.
XX 08-JUL-1999.
XX 24-DEC-1998; 98MO-JP05864.
XX 26-DEC-1997; 97JP-0361022.
XX (KIKK) KIKKOMAN CORP.
XX Hattori N, Murakami S;
XX WPI: 1999-419109/35.
DR P-PSDB; AAY22182.
XX Modified luciferase tolerant to surfactants and useful for assay of
PT intracellular ATP
XX
PS Example 2: Page 34-39; 56pp; English.
XX This sequence encodes a Luciola lateralis luciferase of the invention.
CC The protein is a surfactant-tolerant luciferase which is derived from
CC firefly luciferase by replacement of the glutamic acid residue at
CC position 490 by another amino acid. The luciferase can be used in an
CC assay of intracellular ATP in biological samples containing cells, for
CC example for establishing the presence of cells, and their quantity, in
CC the sample. The method can be applied to foodstuffs, drugs,
CC agrochemicals, beverages and environmental samples. The activity of the
CC surfactant-tolerant luciferase is not lowered by the presence of high
CC concentrations of surfactant and therefore an assay of high accuracy can
CC be carried out in a simple manner.
XX
SQ Sequence 1644 BP: 528 A; 261 C; 349 G; 506 T; 0 other;

Query Match 99.8%; Score 1640.8; DB 20; Length 1644;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 481 agaggtatcaatccatgagacaacttataaaaaaacctccacaaggttccaagga 540
QY 541 tcaagtttaaaactgttagaagtttaacccgaaagacaagttgtcttataatgaactc 600
DB 541 tcaagtttaaaactgttagaagtttaacccgaaagacaagttgtcttataatgaactc 600
QY 601 tgggttcaacccggttttgcgaaggtgtgcgaacttaccatgaaataatgcctactga 660
DB 601 tgggttcaacccggttttgcgaaggtgtgcgaacttaccatgaaataatgcctactga 660
QY 661 ttctccacgttagagatccaatttaagaaacaaagtttccacggacggtctattta 720
DB 661 ttctccacgttagagatccaatttaagaaacaaagtttccacggacggtctattta 720
QY 721 actgttagtaccatccatcatggtttgtgtatgttactacttaggtatctactgt 780
DB 721 actgttagtaccatccatcatggtttgtgtatgttactacttaggtatctactgt 780
QY 781 ggtttcgtatgttcatgttatacgaactttgacgaagagactttttaaaacactgca 840
DB 781 ggtttcgtatgttcatgttatacgaactttgacgaagagactttttaaaacactgca 840
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DB 841 gattacaatgttcaacggttattctgtacacgactttgttgaacttcttaatagaagt 900
QY 901 gaattactcgtataaataatgattatacaattagttgaattgcacgtgcggagacact 960
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DB 961 ttatcctaaagaaattgtgaagctgtgttagaacttttaattccgggtgttcgtcaa 1020
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DB 1021 ggtatgtgtttaaacaagaacaaactctgcgaattatatacacacgggaagcgatataa 1080
QY 1081 ccaggtgtcttgcgaagttgtgcacattttaaaagcaaaagttacgtactgtatct 1140
DB 1081 ccaggtgtcttgcgaagttgtgcacattttaaaagcaaaagttacgtactgtatct 1140
QY 1141 aaaaaaaccttggcccggaacgaacgttggagaagttgtgtaaaggttcctatgtctatg 1200
DB 1141 aaaaaaaccttggcccggaacgaacgttggagaagttgtgtaaaggttcctatgtctatg 1200
QY 1201 aaaggtatgttagataatccagaagcaacaagaagaatcatagatgaagaagttgtgtg 1260
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DB 1501 atgattacgtttgtcagtcgaagtttcaaatgcgaacggtttgcgtgtgtgtgttcgtttt 1560
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Db	1201	aaaggtatgtagataatccaagaacaacaagaalocalatagatgaagaagttgtgttg	1260
OY	1261	caccacgagatatgttgatacttcagatagaanaaacattcttatactgtatcgttg	1320
Db	1261	caccacgagatatgttgatttcagatagaanaaaaacattcttatactgtatcgttg	1320
OY	1321	aagctttlaacaatatacaagaagatatacaagataccaccctgcgaaatagaatctgtctt	1380
Db	1321	aagctttlaacaatatacaagaagatatacaagataccaccctgcgaaatagaatctgtctt	1380
OY	1381	ttgcaacatccaatatattttgtatgcgcggtgtgtgtcgtgtccagatccctataagctgt	1440
Db	1381	ttgcaacatccaatatattttgtatgcgcggtgtgtgtcgtgtccagatccctataagctgt	1440
OY	1441	gaagctccggagagctgttgttctactactaaagaagaatactatctactgaaanaagaata	1500
Db	1441	gaagctccggagagctgttgttctactactaaagaagaatactatctactgaaanaagaata	1500
OY	1501	atgattacggttgcctagtagcaagttccaatgcaaaaagtttcgtgtgtgtgcggttt	1560
Db	1501	atgattacggttgcctagtagcaagttccaatgcaaaaagtttcgtgtgtgtgcggttt	1560
OY	1561	gtggaagaaatgacttaagaagttccctactgttaaaattgcacgtgtaaagaacaattagagaata	1620
Db	1561	gtggaagaaatgacttaagaagttccctactgtgttaaaattgcacgtgtaaagaacaattagagaata	1620
OY	1621	ctgaagaacacagttgtctaagatg	1644
Db	1621	ctgaagaacacagttgtctaagatg	1644

RESULT	4
AAx25718	
ID	AAx25718 standard; cDNA to mRNA; 1644 BP.

AC AAX25718;

DT 21-MAY-1999 (first entry)

DE Firefly luciferase gene #4.

KW Bioluminescent protein; catalytic efficiency; stability; firefly;

KW Photinus pyralis; primer; PCR; amplification; ss.

Luciola lateralis.

synthetic.

WM3902037-AL
FN
XX

21-JAN-1999.
ED
XX

EE 20 JUN 1956, 20MO-0F02730-
XX

[illegible]

XX
XX
XX

XX
XX

Мулдакданил С,
Назлыалия Н,

DR WFL, 1999 120836/10.
DR P-PSDB; AAW99367.

PT New bioluminescent protein with improved properties - has greater

PT	Of natural precursors	of natural precursors	of natural precursors
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2	2	2	2
3	3	3	3
4	4	4	4
5	5	5	5
6	6	6	6
7	7	7	7
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9	9	9	9
10	10	10	10
11	11	11	11
12	12	12	12
13	13	13	13
14	14	14	14
15	15	15	15
16	16	16	16
17	17	17	17
18	18	18	18
19	19	19	19
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31	31	31	31
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96	96	96	96
97	97	97	97
98	98	98	98
99	99	99	99
100	100	100	100

Example 5: Page 35-36; 53pp; Japanese.

CC The invention relates to the generatio

by addition, deletion or substitution of amino acids from a precursor

processes, e.g., directly nucleotides, or by constructing chimeric nucleotides

CC proteins from luciferase genes from e.g. *Luciola cruciata*, *L. lateralis*
CC and *Photinus pyralis*. This sequence represents an example of a mutated
CC luciferase gene of the invention.
XX
SQ Sequence 1644 BP; 528 A; 260 C; 350 G; 506 T; 0 other;

Query Match	99.5%	Score 1636;	DB 20;	Length 1644;
Best Local Similarity	99.7%	Pred. No. 0;		
Matches 1639;	Conservative	0;	Mismatches 5;	Indels 0;
				Gaps 0

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Db	1	atggaaacaactgagaaacgatgaaataattgtagatgctccggaacattttaccatt	60
QY	61	gaagagggaatcgcgcgcgcgcacaaattgctgcgaagtataatgataatgcataatgcacaaacttga	120
Db	61	gaagagggaatcgcgcgcgcgcacaaattgctgcgaagtataatgataatgcataatgcacaaacttga	120
QY	121	gcaattgctttactaacgcacctaaccggtgtcgattatacgtatcgccgaatactatgaa	180
Db	121	gcaattgctttactaacgcacctaaccggtgtcgattatacgtatcgccgaatactatgaa	180
QY	181	aaalcaatcgtctctagggagagcgtttaaagaattatgatttggtttgtttgaaggaagatt	240
Db	181	aaalcaatcgtctctagggagagcgtttaaagaattatgatttggtttgtttgaaggaagatt	240
QY	241	gcgtatgcaatgaaacactgtgaagaattcttatactccgttatagccggtttatata	300
Db	241	gcgtatgcaatgaaacactgtgaagaattcttatactccgttatagccggtttatata	300
QY	301	gggtgcgtgtggtgcctcaacttaagagtttaacactctacgtgagattggtttcaagttta	360
Db	301	gggtgcgtgtggtgcctcaacttaagagtttaacactctacgtgagattggtttcaagttta	360
QY	361	ggcatccttaagcccaacattgtatattggtcttaaaaaagatttagataaagtataact	420
Db	361	ggcatccttaagcccaacattgtatattggtcttaaaaaagatttagataaagtataact	420
QY	421	gtacaaaaacggtaaactgctataaaaaacattgttataatgtggaacgaagtgattat	480
Db	421	gtacaaaaacggtaaactgctataaaaaacattgttataatgtggaacgaagtgattat	480
QY	481	agaagtttcaatccatbtgaacactttttaaaaaaacctccacaaggttttaagga	540
Db	481	agaagtttcaatccatbtgaacactttttaaaaaaacctccacaaggttttaagga	540
QY	541	tcaagttttaaaactgtgaagttaacccgcaagaacaaagtgtcttataatgaact	600
Db	541	tcaagttttaaaactgtgaagttaacccgcaagaacaaagtgtcttataatgaact	600
QY	601	tccgggttcaaccggtttgcccaaaaggtgtgcgaacttactcatgaaatatccgtcaata	660
Db	601	tccgggttcaaccggtttgcccaaaaggtgtgcgaacttactcatgaaatatccgtcaata	660
QY	661	ttttctcagcctagaagatccaatttaatgaaacaaagtttaccaggaacgcgtatttta	720
Db	661	ttttctcagcctagaagatccaatttaatgaaacaaagtttaccaggaacgcgtatttta	720
QY	721	actgtatgataccatccatcaatggttttgtagtgtttactactttaggtacttaactgt	780
Db	721	actgtatgataccatccatcaatggttttgtagtgtttactactttaggtacttaactgt	780
QY	781	ggtttcgtatgtcatgtatgaaatcttgaacgaagactttttaaaaaacgtgaa	840
Db	781	ggtttcgtatgtcatgtatgaaatcttgaacgaagactttttaaaaaacgtgaa	840
QY	841	gattacaatgttcaagcgttatctctgtacagacttggttgcgaattcttaataagaat	900
Db	841	gattacaatgttcaagcgttatctctgtacagacttggttgcgaattcttaataagaat	900
QY	901	gaattactcgaataaataatgattatcaaatatttagttgaattgatactctgycggagcaat	960

```
Db 901 gaattactcgataaataatgattatcaaatltagttgaattgcatctgcygagaccct 960
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XX |||||||
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Db 1081 ccaggtgtctctcgcaaaagtgtgtccattatcttaagaacaaagtatcgatcttgact 1140
OY 1141 aaaaaaacttggcccgacagacgttgagaagtttgttgaaggtctctatgctatg 1200
XX |||||||
XX 1141 aaaaaaacttggcccgacagacgttgagaagtttgttgaaggtctctatgctatg 1200
Db 1141 aaaaaaacttggcccgacagacgttgagaagtttgttgaaggtctctatgctatg 1200
OY 1201 aaaggttatgtatgaataatcagaagaacagaagaatacatagatgaagaagttgttg 1260
XX |||||||
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Db 1201 aaaggttatgtatgaataatcagaagaacagaagaatacatagatgaagaagttgttg 1260
OY 1261 caacacagagatatgtggtatcagatgagaagaaacattcttctatcgtagatcgttg 1320
XX |||||||
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XX |||||||
XX 1321 aagctttaaatacaatacaagaagatacaagtaacacccgtcggaattgaatctgtctt 1380
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OY 1381 ttgcaacatccaataattttttagatccgagctgtgtcgcttcacagatccataagctgtg 1440
XX |||||||
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XX |||||||
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Db 1561 gtggaacgaagtaacttaaaagctcactggttaaatgacgtgtaaaagcaattagaagaata 1620
OY 1621 ctgaagaacacccgtgtgctaagtg 1644
XX |||||||
XX 1621 ctgaagaacacccgtgtgctaagtg 1644
Db 1621 ctgaagaacacccgtgtgctaagtg 1644
```

RESULT 5

AA003257 standard; DNA; 1644 BP.

AA003257;

22-JUL-1990 (first entry)

Luciola lateralis recombinant luciferase gene.

Luciferase; enzyme; ATP; plasmid pHLf7; firefly; ss.

Luciola lateralis.

Key Location/Qualifiers

FT 1..1644

FT /*tag= a

FT /product=Luciferase

FT /EC_number=EC-1.13.12.7

XX EP353464-A.

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PD 07-FEB-1990.
XX
XX 30-JUN-1989; 89EP-0111958.
XX
XX 22-DEC-1988; 88JP-0162402.
XX
XX 01-JUL-1988; 88JP-0162402.
XX
XX (KIKK ) KIKKOMAN CORP.
XX
XX Tatsumi H, Kajiyama N, Nakano E.
XX WPI; 1990-038240/06.
XX P-PSDB; AAR03731.
XX
XX New gene encoding luciferase -
XX derived from Luciola lateralis and expressed in and purified
XX from Escherichia coli genus cells.
XX
XX Claim 3; page 24; 43pp; English.
XX
XX This enzyme is useful for determining ATP levels. It is
XX contained in plasmid pHLf7.
XX
XX Sequence 1644 BP; 529 A; 264 C; 348 G; 503 T; 0 other;
```

Query Match 99.3%; Score 1632.8; DB 11; Length 1644;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1637; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 1 atggaacacatggaagacatgaaatatgtgtatgtatgtctcgtgaacatttaccctatt 60
OY 61 gaagagagatctgtctgagacacattgycgaagtataatgatcgatataatgcaaaacttga 120
XX |||||||
XX 61 gaagagagatctgtctgagacacattgycgaagtataatgatcgatataatgcaaaacttga 120
Db 61 gaagagagatctgtctgagacacattgycgaagtataatgatcgatataatgcaaaacttga 120
OY 121 gaattgctttaaactaaacgacttaacggtgtgcgtatagatagtcggaattataga 180
XX |||||||
XX 121 gaattgctttaaactaaacgacttaacggtgtgcgtatagatagtcggaattataga 180
Db 121 gaattgctttaaactaaacgacttaacggtgtgcgtatagatagtcggaattataga 180
OY 181 aaatcgtgtctctagaagaagccttaagaattatgtgttggtttgaatgaagaatt 240
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```

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QY 661 ttctcagctagaagatcccaattatgaaacccaagttccacgagcacgctatttta 720
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QY 721 actgtaglacatccatcgcacgctgtgtgtagtcttactacttaagctactaacttgt 780
DB 721 actgtaglacatccatcgcacgctgtgtgtagtcttactacttaagctactaacttgt 780
QY 781 ggtttcgtatgtgcacgtaacgaaatttgacgaagagagactttttaaacacactgcaa 840
DB 781 ggtttcgtatgtgcacgtaacgaaatttgacgaagagagactttttaaacacactgcaa 840
QY 841 gattacaagtgtcaagcgttatctctgtacccagcttgtttggaattcctaagaagt 900
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DB 1441 gagcttcgggagagctgtgtgttacttaagaagaagaatcatalgactgtaaaaaagaagta 1500
QY 1501 atggtatcgttctgtcagtcgaagttcaaatgcaaaacgtttggtgtgtgtcgtttt 1560
DB 1501 atggtatcgttctgtcagtcgaagttcaaatgcaaaacgtttggtgtgtgtcgtttt 1560
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DB 1561 gtgacggaagttacctaagaagctcactgtgtaaaattgacggttaagaacatagaagaata 1620
QY 1621 ctgaagaacacagttgtctaagatg 1644
DB 1621 ctgaagaacacagttgtctaagatg 1644

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RESULT 6
AAT63269
ID AAT63269 standard; DNA; 1908 BP.

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XX AC AAT63269;
XX DT 20-MAY-1997 (first entry)
XX DE Gene for firefly luciferase conjugated with 87 aa peptide at 3' end.
XX KW Fusion protein; firefly; luciola lateralis; luciferase; biotinylation;
XX wild type; E.coli; bioluminescence assay; quantification; ligand;
XX receptor; ds.
XX OS Synthetic.
XX FH Key
XX FT CDS 1..1641
XX FT /tag= a
XX FT /note= "encodes firefly portion of fusion protein"
XX FT CDS 1642..1647
XX FT /tag= b
XX FT /note= "sequence encoded by linker used to insert
XX FT sequence encoding biotin peptide to generate
XX FT fusion gene"
XX FT CDS 1648..1908
XX FT /tag= c
XX FT /note= "encodes biotinylated peptide portion of fusion
XX FT protein"
XX PN JP08308578-A.
XX PD 26-NOV-1996.
XX PF 24-APR-1995; 95JP-0098857.
XX PR 14-MAR-1995; 95JP-0054625.
XX PR 27-JUL-1994; 94JP-0193798.
XX PA (KIKR ) KIKROMAN CORP.
XX WP1: 1997-059697/06.
XX DR P-FSDB; AAM12395.
XX PT Fusion protein comprising firefly luciferase and biotinylated
XX PT peptide - useful in a bio-luminescent analytical method for
XX PT quantifying ligands
XX PS Example 7; Page 11-12; 13pp; Japanese.
XX CC This is the nucleotide sequence encoding a novel fusion protein which
XX CC comprises the firefly (luciola lateralis) luciferase protein and an 87
XX CC amino acid biotinylated peptide designated the E.coli biotin carboxy
XX CC carrier protein (BCCP-87). The fusion gene was generated by firstly
XX CC amplifying the sequence encoding the E.coli (BCCP-87) from the E.coli
XX CC genome and inserting the resultant sequence into the 3' end of the
XX CC firefly luciferase gene in plasmid pHLf230. The biotin peptide sequence
XX CC replaces the C-terminal Met residue of the wild type luciferase sequence.
XX CC The plasmid was then introduced into E.coli JM101 for production of the
XX CC fusion protein. The novel protein can be used in bioluminescence assays
XX CC to quantify luciferase ligands which may modulate binding of luciferase
XX CC to its receptor.
XX SQ Sequence 1908 BP; 598 A; 329 C; 426 G; 555 T; 0 other;

```

```

Query Match 99.0%; Score 1628.2; DB 18; Length 1908;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1633; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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DB 1 atggaacacatgagacgatagaataatgtgtatcagttcctgaaccatttaccatt 60
QY 61 gaagaggatcgtcgtgagacacaaattgcgaagatatatgatcgaatgcaaaacttga 120
DB 61 gaagaggatcgtcgtgagacacaaattgcgaagatatatgatcgaatgcaaaacttga 120

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PS Disclosure; Pages 6-7; 10pp; Japanese.

CC The invention claims for a luciferase-lyso-staphin fused gene which
 CC encodes a fused protein in which a peptide part consisting of
 CC luciferase, from *Luciola lateralis*, is connected to a peptide part
 CC consisting of lyso-staphin from *Staphylococcus simulans*. The method
 CC described by the invention can be used to prepare a luciferase-
 CC lyso-staphin fused protein efficiently. The fused protein is useful
 CC for bioluminescence analysis.

XX Sequence 1920 BP; 627 A; 310 C; 407 G; 576 T; 0 other;

Query Match 99.0%; Score 1628.2; DB 19; Length 1920;

Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1633; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 1 atggaacacatgagaaacatgaaatattgtatgtgtccctgaaccatttaccctatt 60
QY 61 gaagaagatctgtgtgagacacattgcgaagtatatgtatgtatgtcgaacattgga 120
Db 61 gaagaagatctgtgtgagacacattgcgaagtatatgtatgtatgtcgaacattgga 120
QY 121 gcaattccttactaacgcacattaccggtgtcgattatcagtaacgcgaatacttgaa 180
Db 121 gcaattccttactaacgcacattaccggtgtcgattatcagtaacgcgaatacttgaa 180
QY 181 aaatcatgctgtctaggagagagcttaagaatatagtttgtttgtttgttgagaagt 240
Db 181 aaatcatgctgtctaggagagagcttaagaatatagtttgtttgtttgttgagaagt 240
QY 241 gcgattagcagtgaaactgtgaaagtattcttattctctgtatgaagccggtttattata 300
Db 241 gcgattagcagtgaaactgtgaaagtattcttattctctgtatgaagccggtttattata 300
QY 301 ggttcggtgtgtgtccaaactaagatattacactacgtgaattgtttccacagtta 360
Db 301 ggttcggtgtgtgtccaaactaagatattacactacgtgaattgtttccacagtta 360
QY 361 ggcattcttaagcacaacattgtattttagttcttaaaaaagattagataaagtataact 420
Db 361 ggcattcttaagcacaacattgtattttagttcttaaaaaagattagataaagtataact 420
QY 421 gtacaaaaaacggttaactgctattataaacattgtttattatgtggcacaagaagtattat 480
Db 421 gtacaaaaaacggttaactgctattataaacattgtttattatgtggcacaagaagtattat 480
QY 481 agaggttaacatcatgacacatttatataaaaaaacacaccacacaagtttcaagaag 540
Db 481 agaggttaacatcatgacacatttatataaaaaaacacaccacacaagtttcaagaag 540
QY 541 tcaagttttaaacctgtagaagtttaacgcgaagaagaagttgctcttataatgaactct 600
Db 541 tcaagttttaaacctgtagaagtttaacgcgaagaagaagttgctcttataatgaactct 600
QY 601 tcgggttaaacccggttgcgaagaaggtgtgcaacttactcctgaacatttgcatacgt 660
Db 601 tcgggttaaacccggttgcgaagaaggtgtgcaacttactcctgaacatttgcatacgt 660
QY 661 ttcttcacgctagaagatccaattatagaaacccaagtttccacgaagcagcgtatttta 720
Db 661 ttcttcacgctagaagatccaattatagaaacccaagtttccacgaagcagcgtatttta 720
QY 721 actgtagtaacatcatcatgtgtttgtatgtttactacttaaggctatcaactgtt 780
Db 721 actgtagtaacatcatcatgtgtttgtatgtttactacttaaggctatcaactgtt 780
QY 781 ggttttgattgtcatgtttaagaatattgacagaagaagctttttaaaacactgaa 840
Db 781 ggttttgattgtcatgtttaagaatattgacagaagaagctttttaaaacactgaa 840

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QY 841 gattacaatgttcaagcgttattcttgcacgacttgttgcatttcttaataagaagt 900
Db 841 gattacaatgttcaagcgttattcttgcacgacttgttgcatttcttaataagaagt 900
QY 901 gaattactgataaataatattatataatattagttgaattgttcattgtgcggagcact 960
Db 901 gaattactgataaataatattatataatattagttgaattgttcattgtgcggagcact 960
QY 961 ttactcaagaagaattgtgaagctgtgtcagcgttttaatttaccgggtgttcgtcaa 1020
Db 961 ttactcaagaagaattgtgaagctgtgtcagcgttttaatttaccgggtgttcgtcaa 1020
QY 1021 gctatgtgtttaacagaacaaacctctgcattatatacacacgggaagcgatgataaa 1080
Db 1021 gctatgtgtttaacagaacaaacctctgcattatatacacacgggaagcgatgataaa 1080
QY 1081 ccaggtgtctctgcgaagaagttgtccattatataaagcaaaagttatcgtatgtatct 1140
Db 1081 ccaggtgtctctgcgaagaagttgtccattatataaagcaaaagttatcgtatgtatct 1140
QY 1141 aaaaaaacttgggcccggaacagcggtgagaagttgtgttaaggggtctctgtatg 1200
Db 1141 aaaaaaacttgggcccggaacagcggtgagaagttgtgttaaggggtctctgtatg 1200
QY 1201 aaaggtatgttaagataatccagaagcaacaagaaatcatagatgaagaagttgtgtg 1260
Db 1201 aaaggtatgttaagataatccagaagcaacaagaaatcatagatgaagaagttgtgtg 1260
QY 1261 cacacagagatactgtgtatatacgtatgaagaagaacattctcttactcgtgatacgttg 1320
Db 1261 cacacagagatactgtgtatatacgtatgaagaagaacattctcttactcgtgatacgttg 1320
QY 1321 aagctttaaatacaatacaagaagatatacaagtaaccacccgcgtgaattgaatactgttct 1380
Db 1321 aagctttaaatacaatacaagaagatatacaagtaaccacccgcgtgaattgaatactgttct 1380
QY 1381 ttgcaacatccaataatttttgaatgcggcggtgtgcgtgtccagatccaataagctgtgt 1440
Db 1381 ttgcaacatccaataatttttgaatgcggcggtgtgcgtgtccagatccaataagctgtgt 1440
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Db 1441 gagcttcgggagcgtgtgtgttgaacttaagaagaatactatgactgtaaaaaagaagta 1500
QY 1501 atgattacgttgtcagtaagtttcaaatgtcaaaacggttgcgtgtgtgttcgtttt 1560
Db 1501 atgattacgttgtcagtaagtttcaaatgtcaaaacggttgcgtgtgtgttcgtttt 1560
QY 1561 gtgacgaaagtacctaagaagttcactgtgttaaatgtacggttaagaacaaattagaagaata 1620
Db 1561 gtgacgaaagtacctaagaagttcactgtgttaaatgtacggttaagaacaaattagaagaata 1620
QY 1621 ctgaagaacacagttgctaag 1641
Db 1621 ctgaagaacacagttgctaag 1641

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RESULT 8

AAAT33850 standard; DNM; 2019 BP.

AAAT33850;

12-NOV-1996 (first entry)

DNA encoding streptavidin/luciferase fusion protein.

Streptavidin; luciferase; fusion protein;

Streptomyces avidinii; *Luciola lateralis*; firefly;

recombinant production; industry; ds.

XX

XX

XX

Key	Location/Qualifiers
FT CDS	1..2019
FT	/*tag= a
PN	JP07289264-A.
XX	
XX	07-NOV-1995.
XX	
XX	27-APR-1994; 94JP-0090275.
XX	
XX	27-APR-1994; 94JP-0090275.
XX	
PA	(KIKK) KIKKOWAN CORP.
XX	
DR	WPI: 1996-015269/02.
XX	P-PSDB; AAM04208.
PT	New mutant streptavidin (SA) gene - fused to a firefly luciferase
XX	gene, for the recombinant prepn. of a SA-FL fused protein
PS	Example 1; Pages 5-6; 12pp; Japanese.
XX	
CC	The present sequence encodes a streptavidin/luciferase fusion
CC	protein, comprising the Streptomyces avidinii streptavidin gene
CC	and the Luciola lateralis (firefly) luciferase gene. The fusion
CC	protein can be prepd. by inserting the recombinant DNA encoding
CC	it into a Escherichia species microbe, culturing the transformed
CC	microbe in a medium and collecting the fusion protein from the
CC	culture. The fusion protein can be used in industry.
XX	
SO	Sequence 2019 BP; 590 A; 412 C; 467 G; 550 T; 0 other;

[illegible]

QY	549	taaacctgtagaagttaaccgcgaagaacaagttgcctctataaigaactcttcggttc	608
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QY	609	aaccggtttgccaaaaggtgtggaacttactctatgaaaatatcgcttactagattttctca	668
Db	984	aaccggtttgccaaaaggtgtggaacttactctatgaaaatatcgcttactagattttctca	1043
QY	669	cgcctagagatccaaatltaaggaaaccagttltaaccgcgcgcgcattlllaactgtagt	728
Db	1044	cgcctagagatccaaatttctatgaaaccagttltaaccgcgcgcgcattttaaactgtagt	1103
QY	729	accattlccatcaggttttgtagtcttactacttaaggctatcctaactgtgttttcg	788
Db	1104	accattlccatcaggttttgtagtcttactacttaaggctatcctaactgtgttttcg	1163
QY	789	tattgtcattgtaacgaattttgcgcgaaggaactttttaaaaccctgcgaatttaaa	848
Db	1164	tattgtcattgtaacgaattttgcgcgaaggaactttttaaaaccctgcgaatttaaa	1223
QY	849	atgttcaagcgttattctctgtaacgaactgttttgcaattcttaataagaaggaattact	908
Db	1224	atgttcaagcgttattctctgtaacgaactgttttgcaattcttaataagaaggaattact	1283
QY	909	cgataaataatgattatcatcaaataggattgaatcgtatcgtgcgcgcacacttatcaa	968
Db	1284	cgataaataatgattatcatcaaataggattgaatcgtatcgtgcgcgcacacttatcaa	1343
QY	969	agaaattgtgtgaagctgtgtgtcgtagacgttttaataccgcggtgtgttcgaagctatgg	1022
Db	1344	agaaattgtgtgaagctgtgtgtcgtagacgttttaataccgcggtgtgttcgaagctatgg	1403
QY	1029	tttaacgaagaacaacctgcgtgaattatatacaaccgcgaagcgatgataaacccgcgtgc	1088
Db	1404	tttaacgaagaacaacctgcgtgaattatatacaaccgcgaagcgatgataaacccgcgtgc	1463
QY	1089	ttcttgcgaagttgttgcattathtaagaacaaagttatcgtatcgtatatactaaaaaac	1148
Db	1464	ttcttgcgaagttgttgcattathtaagaacaaagttatcgtatcgtatatactaaaaaac	1523
QY	1149	tttgggcgcgcgaacgaagctgtgagaagctttgtgtaaaggttcctatgctatagaaggtta	1200
Db	1524	tttgggcgcgcgaacgaagctgtgagaagctttgtgtaaaggttcctatgctatagaaggtta	1583
QY	1209	tgtatgataatccgaagaacaaagaagaatcatatagatgaagaaggttgcgtcacacagg	1266
Db	1584	tgtatgataatccgaagaagaagaagaatcatatagatgaagaaggttgcgtcacacagg	1643
QY	1269	agatatgtggtattacgaatgaagaanaaacattccttatcgttgaatcgttttgaagcttt	1328
Db	1644	agatatgtggtattacgaatgaagaanaaacattccttatcgttgaatcgttttgaagcttt	1703
QY	1329	aatcaatacagaagatatacaagttaccacctgcgtgaattagaatcgtttcttttgcaca	1388
Db	1704	aatcaatacagaagatatacaagttaccacctgcgtgaattagaatcgtttcttttgcaca	1763
QY	1389	tccaataatttttgaatgcgcgcggttgcgttgcgttccaagatccataagcgtgcgcgcctcc	1448
Db	1764	tccaataatttttgaatgcgcgcggttgcgttgcgttccaagatccataagcgtgcgcgcctcc	1823
QY	1449	gggaagctgttcttacttaagaagaagaatactatgactgaataaagaagtaatgtagta	1508
Db	1824	gggaagctgttcttacttgaataaagaatactatgactgaataaagaagtaatgtagta	1883
QY	1509	cgttgcctagttcaagttccaatgtcaaaaagctttgcgtgtgtgtgttcgcttttgcgcga	1566
Db	1884	cgttgcctagttcaagttccaatgtcaaaaagctttgcgtgtgtgtgtgttcgcttttgcgcga	1943
QY	1569	agttacctaaaggtctcaactgtgtaaaatttgcgttgaagaacattagaagaaatacttgaaga	1628
Db	1944	agttacctaaaggtctcaactgtgtaaaatttgcgttgaagaacattagaagaaatacttgaaga	2003
QY	1629	accagtttctaagctg 1644	

Db 2004 accagttgctaagatg 2019
|||||
RESULT 9
ID AAT33851 standard; DNA: 2055 BP.
AC AAT33851:
XX
XX
XX 12-NOV-1996 (first entry)
XX
XX DNA encoding mutant streptavidin/Luciferase fusion protein.
XX
XX Mutant: streptavidin: luciferase: fusion protein:
KM Streptomyces avidinii; Luciola lateralis; firefly;
KM recombinant production; Industry; ds.
XX
XX Synthetic.
FH Key 1.2055 Location/Qualifiers
FT CDS /tag= a
FT /note= "STOP codon absent"
PN JP07289264-A.
XX 07-NOV-1995.
XX
XX 27-APR-1994; 94JP-0090275.
XX
XX 27-APR-1994; 94JP-0090275.
XX
XX (KIKK) KIKKOMAN CORP.
XX
XX WPI: 1996-015269/02.
DR P-PSDB; AAM04208.
XX
XX
PT New mutant streptavidin (SA) gene - fused to a firefly luciferase
PT gene, for the recombinant prepn. of a SA-FL fused protein
PS Claim 1; Pages 7-8; 12pp; Japanese.
XX
XX The present sequence encodes a mutant streptavidin/luciferase
CC fusion protein, comprising a mutant Streptomyces avidinii
CC streptavidin gene and the Luciola lateralis (firefly) luciferase
CC gene. The fusion protein can be prepd. by inserting the
CC recombinant DNA encoding it into a Escherichia species microbe,
CC culturing the transformed microbe in a medium and collecting the
CC fusion protein from the culture. The fusion protein can be used
CC in industry.
XX
XX Sequence 2055 BP; 603 A; 418 C; 474 G; 560 T; 0 other;
SQ
Query Match 98.5%; Score 1620; DB 17; Length 2055;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 600 ctgtctagagagagccttaagaattatggttctgtctgtatggaagaatgcgtatg 659
QY 249 cagtgaaaacitggaagaattcttattccctgtattgaacgggttatttataggttcg 308
Db 660 cagtgaaaacitggaagaattcttattccctgtattgaacgggttatttataggttcg 719
QY 309 tctgtcccaactaattgaatttaccctctacgttgatgtgttcacagtlttaggcattc 368
Db 720 tctgtcccaactaattgaatttaccctctacgttgatgtgttcacagtlttaggcattc 779
QY 369 taagccaacaattgtattttagttcttaaaaaaagattagataaagttaactgtcaaaa 428
Db 780 taagccaacaattgtattttagttcttaaaaaaagattagataaagttaactgtcaaaa 839
QY 429 aacggttaactgtatttaaacattgtttatattggaacgaagtggtttatagaagtt 488
Db 840 aacggttaactgtatttaaacattgtttatattggaacgaagtggtttatagaagtt 899
QY 489 tcaatccatggaacacttatttaaaaaaaacacatccacaaggtttcaagaagttcaagtt 548
Db 900 tcaatccatggaacacttatttaaaaaaaacacatccacaaggtttcaagaagttcaagtt 959
QY 549 taaactgtagaagtttaacccgaagaagaagttgctcttaataagaaactcttggttc 608
Db 960 taaactgtagaagtttaacccgaagaagaagttgctcttaataagaaactcttggttc 1019
QY 609 aaccggtttgccaagaagtggttcaacttactatgaataaatatcgtcaactagatttcc 668
Db 1020 aaccggtttgccaagaagtggttcaacttactatgaataaatatcgtcaactagatttcc 1079
QY 669 cgtctagatgccaatltatggaacccaagtttcacacgaacggtctatttactgtatg 728
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QY 1209 ttttagataatccagaagcaacaagaaatcatagataagaaggttggttgcacaaggt 1268
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QY 1269 agatattgggttattagatgaagaagaacattcttattcgttgatcgtttgaagcttt 1328
Db 1680 agatattgggttattagatgaagaagaacattcttattcgttgatcgtttgaagcttt 1739


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QY 851 gtcaacgcttattctgtacacgacttctgcaattcttaataagaatgaactctg 910
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QY 911 ataatatgattatcaaatattagtgaaatgacatcgcgagacacttactaaag 970
    |||||||
Db 971 ataatatgattatcaaatattagtgaaatgacatcgcgagacacttactaaag 1030
QY 971 aaattgtgaagctgtgtgacagcgttttaattaccgggtgttcgaaggtatggt 1030
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QY 1091 ctggcaaatgtgtgcaattatttaagcaaatgtatcgacttgaactactaaact 1150
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QY 1211 tagataatccagaagcacacagaagaatcatagatgaagaaggtgtgtcacacagag 1270
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QY 1271 atattgtgtatcgatgaagaagaacattcttactgtgactgttgaagtccttaa 1330
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QY 1331 tcaaatcaagaagatcaatcaatgtaacacatctgtaattagaatgtgtcttttcaacac 1390
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Db 1391 tcaaatcaagaagatcaatcaatgtaacacatctgtaattagaatgtgtcttttcaacac 1450
QY 1391 caaatattttgtatgcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1450
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QY 1451 gactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1510
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Db 1511 gactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1570
QY 1511 ttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1570
    |||||||
Db 1571 ttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1630
QY 1571 taactaaaggtctcaactgtgtaaatgtacgtaagaacatlagagaataactgaagaac 1630
    |||||||
Db 1631 taactaaaggtctcaactgtgtaaatgtacgtaagaacatlagagaataactgaagaac 1690
QY 1631 caagtgtctgaagatg 1644
    |||||||
Db 1691 caagtgtctgaagatg 1704

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RESULT 11

AAV23595 standard; cDNA to mRNA; 1704 BP.

AAV23595;

16-JUL-1998 (first entry)

Antibody-Firefly Luciferase fusion protein gene.

Firefly Luciferase; antibody-Luciferase fusion protein; ds.

Luciola cruciata.

Key Location/Qualifiers

CDS 1..1704

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FT          /*tag= a
FR          /note= "no stop codon given"
PN          JP09187281-A.
PD          22-JUL-1997.
PF          09-JAN-1996; 96JP-0001812.
PR          09-JAN-1996; 96JP-0001812.
PS          (KIKK ) KIKKOMAN CORP.
DR          WPI; 1998-275089/25.
CC          P-PSDB; AAM53883.
PT          Antibody-firefly luciferase fused protein - and related products
PT          i.e. firefly luciferase fused gene, recombinant DNA and its
PT          preparation
PS          Disclosure: Page 10-11; 17pp; Japanese.
CC          This sequence encodes a fusion protein of the invention. The protein is
CC          a antibody-firefly luciferase fusion protein, in which an antibody part
CC          consisting of a peptide having antibody activity is combined with an
CC          enzyme part consisting of firefly luciferase.
XX          Sequence 1704 BP; 541 A; 275 C; 361 G; 527 T; 0 other:

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Query Match          98.5%; Score 1619.6; DB 19; Length 1704;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1625; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 251 gctcagaagaagccttaagaatattggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 310
QY 251 gtgaagaactgtgaagaactcttattcctgtattagccggttatttattaggtgtcggtg 310
    |||||||
Db 311 gtgaagaactgtgaagaactcttattcctgtattagccggttatttattaggtgtcggtg 370
QY 311 tggctccaactaatgagatttacaactctacgtgaattgtgttcaacagtttaggcactcta 370
    |||||||
Db 371 tggctccaactaatgagatttacaactctacgtgaattgtgttcaacagtttaggcactcta 430
QY 371 agccaacaattgtatttatttcttaaaaaagattagataaagttataactgtcaaaaaa 430
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QY 431 cgttaactgtctattaaacacattgtattattgagacgaagaagtgtattatagaattatc 490
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Db 491 cgttaactgtctattaaacacattgtattattgagacgaagaagtgtattatagaattatc 550
QY 491 aatcgaatgacacatttataaaaaaacacccaagaagtttcaagaagatcaagtttta 550
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QY 551 aaactgtagaagtttaacgcgaagaagaagttgtcttataatgaacaccttggttcaa 610
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Db 611 aaactgtagaagtttaacgcgaagaagaagttgtcttataatgaacaccttggttcaa 670

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QY	611	ccggtttgcgaagaagtgvtgtaacttactctcatgtaataatctgctcaactagattttctccag	670
Db	671	ccgggtttgcgaagaagtgvtgtaacttactctcatgtaaaaaatttggttccagcgttttttccag	730
QY	671	ctagagatcccaattatalgaaacaaagttccacagacaggtctattttaactgtgtac	730
Db	731	ctagagatcccaattatalgaaacaaagtttccacagacaggtctattttaactgtgtac	790
QY	731	catlccatcatggttttgtatgttctactcttaagctctactaactgtgylttcgtta	790
Db	791	catlccatcatggttttgtatgttctactcttaagctctactaactgtgylttcgtta	850
QY	791	ttgtcatgtttagcaaaatttgacagaagaagctttttaaaaacacgcgaagtttccaat	850
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QY	911	ataaatgatgatttccaanttagttgaattgcatcttgycgagacacttattctaaag	970
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QY	971	aaatgtggaagcgtgtgttagagacggttttattacccgggtgtgttgcgaagctatggt	1030
Db	1031	aaatgtggaagcgtgtgttagagacggttttattacccgggtgtgttgcgaagctatggt	1090
QY	1031	taacagaaacaacctctgccaattattatccaccggagaagcgatgataaaccagtgctt	1090
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QY	1091	ctggaacaaggtgtgccaattatttaagaacaaagtttgcgatctgtgatactaaaaaact	1150
Db	1151	ctggaacaaggtgtgccaattatttaagaacaaagtttgcgatctgtgatactaaaaaact	1210
QY	1151	ttgggcccgacagacgctgvgagaagtgtgtglaaaggttccatgcttactgtaaaaggtttag	1210
Db	1211	ttgggcccgacagacgctgvgagaagtgtgtglaaaggttccatgcttactgtaaaaggtttag	1270
QY	1211	tagataatccgaagcagaacagaagaaatctcatagataagaaggtgtgttcacacagag	1270
Db	1271	tagataatccgaagcagaacagaagaaatctcatagataagaaggtgtgttcacacagag	1330
QY	1271	atatgtggttactacgaatgaaagaacaaactcttcttactcgtgtaacgtttgtaagctttaa	1330
Db	1331	atatgtggttactacgaatgaaagaacaaactcttcttactcgtgtaacgtttgtaagctttaa	1390
QY	1331	tcaaatatacaagatatacatcaagttacacaccgtgcgtaattagaatcgttcttcttgcacac	1390
Db	1391	tcaaatatacaagatatacatcaagttacacaccgtgcgtaattagaatcgttcttcttgcacac	1450
QY	1391	caaatatttttgatgacccggcgttgcgtgcgtcttccagatccctatagcttggtagcttcgg	1450
Db	1451	caaatatttttgatgacccggcgttgcgtgcgtcttccagatccctatagcttggtagcttcgg	1510
QY	1451	gagcgtgtgtgttactctaaagaagaacatactatgactgaaagaagatgatactgatacg	1510
Db	1511	gagcgtgtgtgttactctgtaaaagaagaacatactatgactgaaagaagatgatactgatacg	1570
QY	1511	ttgtgtatgcaagtttcaaatgcaaaacggttttggtgtgtgtgttcggttttggagcgaag	1570
Db	1571	ttgtgtatgcaagtttcaaatgcaaaacggttttggtgtgtgtgtgttcggttttggagcgaag	1630
QY	1571	taccataaaggtctcaactcagtgtaaaatgacgtgataaagaattagaaataactcgaagaac	1630
Db	1631	taccataaaggtctcaactcagtgtaaaatgacgtgataaagaattagaaataactcgaagaac	1690
QY	1631	caagttgtctaagaagtg	1644
Db	1691	caagttgtctaagaagtg	1704

ID	AAV23580	standard; CDNA to mRNA; 2364 BP.
AAV23580;		
16-JUL-1998	(first entry)	
Antibody-Firefly Luciferase fusion protein gene.		
Firefly Luciferase; antibody-luciferase fusion protein; ds.		
Luciola cruciata.		
Key	Location/Qualifiers	
CDS	1..2364	
FT	/*tag= a	
FT	/transl_except= (pos: 670..672, aa: Glu)	
FT	/transl_except= (pos: 739..741, aa: Trp)	
FT	/transl_except= (pos: 1369..1371, aa: Ala)	
FT	/note= "no stop codon given"	
JP09187281-A.		
22-JUL-1997.		
09-JAN-1996;	96JP-0001812.	
09-JAN-1996;	96JP-0001812.	
(KIKK) KIRKOMAN CORP.		
WPI, 1998-275089/25.		
P-PSDB; AAM53882.		
Antibody-firefly Luciferase fused protein - and related products		
i.e. firefly luciferase fused gene, recombinant DNA and its		
preparation		
Disclosure; Page 13; 17pp; Japanese.		
This sequence encodes the fusion protein of the invention. The protein is		
a antibody-firefly luciferase fusion protein, in which an antibody part		
consisting of a peptide having antibody activity is combined with an		
enzyme part consisting of firefly luciferase.		
Sequence 2364 BP; 697 A; 444 C; 559 G; 664 T; 0 other;		
Query Match	98.4%; Score 1618.4; DB 19; Length 2364;	
Best Local Similarity	99.3%; Pred. No. 0;	
Matches 1625; Conservative	0; Mismatches 11; Indels 0; Gaps 0;	
9	cattgagaagcgtgtaaatatgttatggtctctgaaccatttaccctatgaagag	68
1	lcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt	788
729	cctcgagaagcgtgtaaatatgttatggtctctgaaccatttaccctatgaagag	788
69	atctgctggaagcacaattgctgcaaglatatglatcgatatgcaaaacttgagcaattgc	128
789	atctgctggaagcacaattgctgcaaglatatglatcgatatgcaaaacttgagcaattgc	848
129	tttacttaagcgaacttaccggtgtgtgatattacgacgcgaataactttagaaaaatcatc	188
849	tttacttaagcgaacttaccggtgtgtgatattacgacgcgaataactttagaaaaatcatc	908
189	ctgtctagagagagcgtttaaagaattatgatttggcttctgtagaggaagattgcgtatc	248
909	ctgtctagagagagcgtttaaagaattatgatttggcttctgtagaggaagattgcgtatc	968
249	cagtgaaaaactgtggaagaattccttattcctglatatgacgcggttattattataggtgcg	308
969	cagtgaaaaactgtggaagaattccttattcctglatatgacgcggttattattataggtgcg	1028

QY 309 tctggtcccaactaagtattacatctacgtgaattgtgtccacgttttagcatctc 368
 Db 1029 tctggtcccaactaagtattacatctacgtgaattgtgtccacgttttagcatctc 1088
 QY 369 taagccaacattgttattagttcttaaaaaagagatagataaagtataactgtcaaaa 428
 Db 1089 taagccaacattgttattagttcttaaaaaagagatagataaagtataactgtcaaaa 1148
 QY 429 aacggttaactgtatttaaacattgttatattgacgcgcaaaagtgtatataaggtta 488
 Db 1149 aacggttaactgtatttaaacattgttatattgacgcgcaaaagtgtatataaggtta 1208
 QY 489 tcaatccagagcaacttatttaaaaaaacatccacaaagttccaagaatcaagt 548
 Db 1209 tcaatccagagcaacttatttaaaaaaacatccacaaagttccaagaatcaagt 1268
 QY 549 taaactgtagaagttaaccgcgaagaacagttgtctctataatgaactctcggttc 608
 Db 1269 taaactgtagaagttaaccgcgaagaacagttgtctctataatgaactctcggttc 1328
 QY 609 aacgggttgcgaagaagtgatcaacttaactatgaanaatatacgtccactagaatttcca 668
 Db 1329 aacgggttgcgaagaagtgatcaacttaactatgaanaatatacgtccactagaatttcca 1388
 QY 669 cgttagagatccaattataggaacccaagttccacagcagcggtattttaactgtagt 728
 Db 1389 cgttagagatccaattataggaacccaagttccacagcagcggtattttaactgtagt 1448
 QY 729 accatccatcagtggtttgtatgttttaacttaacttaggtatacttaactgtgtttcg 788
 Db 1449 accatccatcagtggtttgtatgttttaacttaacttaggtatacttaactgtgtttcg 1508
 QY 789 tattgtcatgttaacgaanaatttgacgaagaagctttttaaaaaacatgcgaagtataca 848
 Db 1509 tattgtcatgttaacgaanaatttgacgaagaagctttttaaaaaacatgcgaagtataca 1568
 QY 849 atgttcaagcgttatctctgttacccagcttgtttgcaacttctaataagaagtgaaattact 908
 Db 1569 atgttcaagcgttatctctgttacccagcttgtttgcaacttctaataagaagtgaaattact 1628
 QY 909 cgaataaatatgtatttaacaatttagtgaattgtgcatctgacgcgagcaccattatctaa 968
 Db 1629 cgaataaatatgtatttaacaatttagtgaattgtgcatctgacgcgagcaccattatctaa 1688
 QY 969 agaaattgtgtgaagcgtgtgtctagaacggttttaattaccgggtgtgtcgaagctatg 1028
 Db 1689 agaaattgtgtgaagcgtgtgtctagaacggttttaattaccgggtgtgtcgaagctatg 1748
 QY 1029 ttttaacagaacaacactctgtcaattatatacaccggaagcgatagataaacacaggtgc 1088
 Db 1749 ttttaacagaacaacactctgtcaattatatacaccggaagcgatagataaacacaggtgc 1808
 QY 1089 ttctggcgaagtgtgcatattttaaagcaaaagtatcgcattctgtatctataaaaaaac 1148
 Db 1809 ttctggcgaagtgtgcatattttaaagcaaaagtatcgcattctgtatctataaaaaaac 1868
 QY 1149 ttgggcccgaagaacggtggaagaatttgtgtaaaggtctctatgctataaaggtta 1208
 Db 1869 ttgggcccgaagaacggtggaagaatttgtgtaaaggtctctatgctataaaggtta 1928
 QY 1209 tgttagtaataccgaagcaacaagaagaatcatagatgaagaaggtgtgtgtcacacag 1268
 Db 1929 tgttagtaataccgaagcaacaagaagaatcatagatgaagaaggtgtgtgtcacacag 1988
 QY 1269 agatattgggtattacgatgaagaanaaacattctttatcgttgaacggtttgaagctt 1328
 Db 1989 agatattgggtattacgatgaagaanaaacattctttatcgttgaacggtttgaagctt 2048
 QY 1329 aatcaaatataaagatataagttaccacgtgtgaattagaatctgtctttttgcaaca 1388
 Db 2049 aatcaaatataaagatataagttaccacgtgtgaattagaatctgtctttttgcaaca 2108

QY 1389 tccaaatattttgaatgcggcggttgcgtggttccagatccataagctgtgaagcttc 1448
 Db 2109 tccaaatattttttgagtcggcggttgcgtggttccagatccataagctgtgaagcttc 2168
 QY 1449 gggagcgttctgttacttaagaagaataatcatatgacgtgaagaagaatgaatgattta 1508
 Db 2169 gggagcgttctgttacttaagaagaataatcatatgacgtgaagaagaatgaatgattta 2228
 QY 1509 cgttgcataagtttccaattgcaaaacggttgcgtggtgtgtccgtttttgtgacga 1568
 Db 2229 cgttgcataagtttccaattgcaaaacggttgcgtggtgtgtccgtttttgtgacga 2288
 QY 1569 agtaactaaaggtctcaactgtgttaaatgacgtgaagaacattagaagaataactgaagaa 1628
 Db 2289 agtaactaaaggtctcaactgtgttaaatgacgtgaagaacattagaagaataactgaagaa 2348
 QY 1629 accagttgctaagatg 1644
 Db 2349 accagttgctaagatg 2364

RESULT 13

AAK25717 standard; cDNA to mRNA; 1656 BP.

ID AAK25717 standard; cDNA to mRNA; 1656 BP.
 XX AAK25717;
 AC AAK25717;
 XX 21-MAY-1999 (first entry)
 DT 21-MAY-1999 (first entry)
 XX Firefly luciferase gene #3.
 DE Firefly luciferase gene #3.
 KW Bioluminescent protein; catalytic efficiency; stability; firefly;
 KW luciferase; chimeric; luciola cruciata; luciola lateralis;
 KW Photinus pyralis; primer; PCR; amplification; ss.
 XX Chimeric - Luciola lateralis.
 OS Chimeric - Photinus pyralis.
 XX MO9902697-A1.
 PN 21-JAN-1999.
 PD 21-JAN-1999.
 XX 30-JUN-1998; 98WO-JP02936.
 PF 08-JUL-1997; 97US-0051917.
 PR (KIKK) KIKKOMAN CORP.
 XX Hirokawa K, Kajiyama N, Murakami S;
 PI WPI: 1999-120898/10.
 DR P-PSDB; AAM99366.
 DR New bioluminescent protein with improved properties - has greater
 PT catalytic efficiency and stability and is obtained by modification
 PR of natural precursors
 XX Example 3; Page 30-31; 53pp; Japanese.
 PS The invention relates to the generation of bioluminescent proteins with
 CC improved catalytic efficiency and stability. The proteins are generated
 CC by addition, deletion or substitution of amino acids from a precursor
 CC protein e.g. firefly luciferases, or by constructing chimeric luciferase
 CC proteins from luciferase genes from e.g. luciola cruciata, L. lateralis
 CC and Photinus pyralis. This sequence represents an example of a chimeric
 CC luciferase gene of the invention.
 XX Sequence 1656 BP; 529 A; 283 C; 366 G; 478 T; 0 other;

Query Match 90.7%; Score 1490.4; DB 20; Length 1656;
 Best Local Similarity 94.7%; Pred. No. 0;
 Matches 1542; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

PT In E. coli, obtaining a stable and highly active prod.

XX Claim 2; fig 3; 35pp; English.

CC The sequence was obtd. from cDNA prep'd. from mRNA isolated from
CC L. cruciata tails. The DNA can be incorporated into vectors for
CC transformation of E. coli JM 1010.

XX Sequence 1644 BP; 529 A; 276 C; 338 G; 501 T; 0 other;

Query Match 82.6%; Score 1357.6; DB 10; Length 1644;

Best Local Similarity 89.1%; Pred. No. 0; Matches 1465; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

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Db 61 gaagaggagatcgtgagacaaatctgcaagatataatgcatatgcaaaacttga 120
QY 121 gcaattcctttaaagcaactaccggtgctcgattatagcgcgcgaatacttga 180
Db 121 gcaattcctttaaagcaactaccggtgctcgattatagcgcgcgaatacttga 180
QY 181 aaatcatgctctagagagagcttaagaataatgctgtgtgttgaatgagaat 240
Db 181 aaatcatgctctagagagagcttaagaataatgctgtgtgttgaatgagaat 240
QY 241 gcttatgagctgaaactgtgaagatctcttaacttatagccggtttattata 300
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QY 301 ggttcggtgtgctccaactatgagatctacacctacgctgagctgttcaagtt 360
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QY 361 ggcattcctaaagcaaatctgtatctgtcttaaaaaagagatagataagttact 420
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QY 421 gtacaaaaaacgtaactgctataaaccattgttatatgagacgaagtgatatt 480
Db 421 gtacaaaaaacgtaactgctataaaccattgttatatgagacgaagtgatatt 480
QY 481 agaggtatcaatcactgagacactttataaaaaaacactccacaaggtttcaaga 540
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QY 541 tcaagttttaaaactgtagaagtttaacgcgaagaagaagttgctcttataatct 600
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Db 781 ggttcgctatgcatgttaacgaatattacgaagaagactttttaaaacctgaa 840
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Db 841 gattacaagcttcaagcttattctgtacgaacttgtttgcaatcttaacaaagt 900
QY 901 gattactcgataaataatattatcatcaaatctgaattggaattgcactcgtgcgaacct 960
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Db 1441 gagcttcgggagctgtgttgaatcttaagaagaagaatctcatgactgtaaaagaaga 1500
QY 1501 atgattacgttgcagtaagtttcaaatgcaaaacgcttgcgtgtgtgtcgtttt 1560
Db 1501 atgattacgttgcagtaagtttcaaatgcaaaacgcttgcgtgtgtgtcgtttt 1560
QY 1561 gtgacgaagttactctaaggtctcactgttaaatgtgacggtcaagaatgagaata 1620
Db 1561 gtgacgaagttactctaaggtctcactgttaaatgtgacggtcaagaatgagaata 1620
QY 1621 ctgaagaaccagttgctaagatg 1644
Db 1621 ctgaagaaccagttgctaagatg 1644
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RESULT 15
AA003801
ID AA003801 standard; cDNA; 1644 BP.
XX
AC AA003801;
XX
AC
XX
DT 22-AUG-1990 (first entry)
DT 26-FEB-1993 (revised entry)
XX
DE Recombinant luciferase gene.
XX
KW Luciferase; ATP; E. coli; photon; ds.
XX
OS Synthetic.
XX
PN JF02065780-A.
XX
PD 06-MAR-1990.

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OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 19:29:53 : Search time 113.65 Seconds
(without alignments)
3553.203 Million cell updates/sec

Title: US-09-581-241-5
Perfect score: 1644
Sequence: 1 atggaacaatgagaacga.....agaaccagtgctaagatg 1644

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/1na/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/1na/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/1na/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/1na/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/1na/PCRTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1636	99.5	1644	1	US-07-903-047-7 Sequence 7, Appl
2	1636	99.5	1644	3	US-09-111-752-13 Sequence 13, Appl
3	1636	99.5	1644	4	US-09-380-061B-15 Sequence 15, Appl
4	1628.2	99.0	1908	1	US-08-460-934-8 Sequence 8, Appl
5	1628.2	99.0	1908	2	US-08-782-118-8 Sequence 8, Appl
6	1619.6	98.5	1704	1	US-08-460-934-5 Sequence 5, Appl
7	1619.6	98.5	1704	2	US-08-782-118-5 Sequence 5, Appl
8	1357.6	82.6	1644	1	US-07-675-211-1 Sequence 1, Appl
9	1357.6	82.6	1644	1	US-07-903-047-1 Sequence 1, Appl
10	1357.6	82.6	1644	1	US-08-076-042-1 Sequence 1, Appl
11	1357.6	82.6	1644	2	US-08-757-046A-3 Sequence 3, Appl
12	1357.6	82.6	1644	3	US-09-447-208-3 Sequence 3, Appl
13	1357.6	82.6	1644	3	US-09-135-988-3 Sequence 3, Appl
14	1357.6	82.6	1644	4	US-09-277-716-3 Sequence 3, Appl
15	1357.6	82.6	1644	4	US-08-597-274A-3 Sequence 3, Appl
16	1357.6	82.6	1644	4	US-09-380-061B-13 Sequence 13, Appl
17	1264.8	76.9	1656	3	US-09-111-752-8 Sequence 8, Appl
18	1042.4	63.4	1656	3	US-09-111-752-6 Sequence 6, Appl
19	1042.4	63.4	1656	3	US-09-111-752-9 Sequence 9, Appl
20	1014.4	61.7	2009	4	US-09-380-061B-17 Sequence 17, Appl
21	817.2	49.7	1725	4	US-09-380-061B-19 Sequence 19, Appl
22	747.4	45.5	5427	3	US-09-282-996-2 Sequence 2, Appl
23	746.8	45.4	1811	3	US-08-867-352-22 Sequence 22, Appl
24	746.8	45.4	5789	3	US-08-862-431-32 Sequence 32, Appl
25	746.8	45.4	5791	3	US-08-862-431-31 Sequence 31, Appl
26	746.8	45.4	5793	3	US-08-862-431-29 Sequence 29, Appl
27	746.8	45.4	5793	3	US-08-862-431-30 Sequence 30, Appl

28	746.8	45.4	5818	2	US-08-536-559A-3 Sequence 3, Appl
29	746.8	45.4	5819	2	US-08-536-559A-2 Sequence 2, Appl
30	746.8	45.4	5819	3	US-08-862-431-27 Sequence 27, Appl
31	746.8	45.4	5819	3	US-08-862-431-28 Sequence 28, Appl
32	746.8	45.4	5938	2	US-08-536-559A-4 Sequence 4, Appl
33	746.8	45.4	6092	2	US-08-536-559A-1 Sequence 1, Appl
34	746.8	45.4	6092	3	US-08-862-431-26 Sequence 26, Appl
35	746.8	45.4	11616	1	US-08-196-259-2 Sequence 2, Appl
36	745.6	45.3	1722	4	US-09-380-061B-1 Sequence 1, Appl
37	745.2	45.3	1650	1	US-08-354-240A-1 Sequence 1, Appl
38	745.2	45.3	2445	1	US-08-122-520C-8 Sequence 8, Appl
39	745.2	45.3	5620	2	US-08-793-170-21 Sequence 21, Appl
40	745.2	45.3	5620	3	US-08-892-873-21 Sequence 21, Appl
41	745.2	45.3	5620	4	US-09-334-765A-21 Sequence 21, Appl
42	745.2	45.3	5620	4	US-09-356-575E-21 Sequence 21, Appl
43	745.2	45.3	5620	4	US-09-333-820-21 Sequence 21, Appl
44	745.2	45.3	6044	1	US-08-316-950-18 Sequence 18, Appl
45	745.2	45.3	6044	5	PCT-US95-12642-18 Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-07-903-047-7
Sequence 7, Application US/07903047
Patent No. 5229285
GENERAL INFORMATION:
APPLICANT: Kajiyama, Naoki
TITLE OF INVENTION: Thermostable Luciferase of Firefly,
TITLE OF INVENTION: Thermostable Luciferase Gene of Firefly, No. 5229285el Reco
TITLE OF INVENTION: DNA And Process for The Preparation of Thermostable
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,047
FILING DATE: 19920623
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1644 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA to mRNA
US-07-903-047-7

Query Match 99.5%; Score 1636; DB 1; Length 1644;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 421 gtacaaaacggttaactgctatataaacatgttataatgtgacagcaagtgtat 480
 Db 421 GTACAAAACGGTAACTGCTATATAAACCATGTGTATATGTGACAGCAAGTGTATN 480
 Qy 481 aagsgttatcaatcactgagcaacttataaaaaaacacacccacacaggtttcaagga 540
 Db 481 AGAGGTTATCAATCCATGACCACTTTATTAATAAAAAAACACTCCACAGGTTCAAGGA 540
 Qy 541 tcaagttttaaactgtagaagtttaacccgaagaacaggtgtcttataatgaactct 600
 Db 541 TCAAGTTTAAACTGTAGAAGTTAAACCCGAAGAACAAAGTGTCTTTAATAAGAACTCT 600
 Qy 601 tcgggttcaaccggtttgcaaaaaggtgtcaacttactatcaataatcgtcactaga 660
 Db 601 TCGGGTTCAACCGGTTTGCCAAAAGGTGTCACTTACTATCAATAAATTTGGTCACGGC 660
 Qy 661 tttctcaagctagagatcccaattatggaacaaagtttaccagagcagctatttta 720
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 Db 721 ACTGTATACCATTCCTCAATGTTGGTATGTATGTTACTTACCTTACCTTACCTTGT 780
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 Db 781 GGTTCGTATGTGTCATGTTAAGCAATTTGACGAGAGACTTTTAAACAACTGCAC 840
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 Qy 901 gaattactgataaataatgatttataaataatgattgaaattgactgtgcggaagacct 960
 Db 901 GAATTACTGATAAATAATGATTATCAAAATTTAGTTGAATTCATCTGTGCGAGACCT 960
 Qy 961 ttacttaagaatgtgtgagactgtgtctagacgctttaaaccggtgtctgcga 1020
 Db 961 TTACTTAAGAATGTGTGAGCTGTGTGCTAGACGTTTATTTACCGGCTGTGTGCAC 1020
 Qy 1021 ggtctatgtttaaagaacaacactctgcaattattcaacacgggaaggcgtatga 1080
 Db 1021 GGCTATGTGTTAAACAGAAACACCTCTGCAATTTATTCACACCGGAAGCGATGAT 1080
 Qy 1081 ccaggtctcttcgcaagaagtgtgccaattttaaagaacaagttacgtctgttact 1140
 Db 1081 CCAGGTCTCTTGCAAGTGTGTGCCATTTATTTAAACCAAAAGTTATCGATCTTGACT 1140
 Qy 1141 aaaaaaaccttggcccgcaacagcgtggaagttgtgttaaagggtccatgtctatg 1200
 Db 1141 AAAAAAATTTGGGCCCGCAACAGCGTGAAGTTGTGTAAAGGCTCTATGCTTATG 1200
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 Db 1201 AAAGGTATGTAGTATATCCAGAAGCAACAGAAATCATAGATGAAGAAGTTGTTG 1260
 Qy 1261 caaccagagatattgtgtttaaagaaagaaacattcttactgtgagtcgtttg 1320
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Db 1501 ATGGATTAGCTGTAGTCACAACTTCAATGCAAAACGTTGCGGTGTCGTTT 1560
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RESULT 6
 US-08-460-934-5
 ; Sequence 5, Application US/08460934
 ; Patent No. 5814465
 ; GENERAL INFORMATION:
 ; APPLICANT: TATSUMI, HIROKI
 ; APPLICANT: FUKUDA, SATOSHI
 ; APPLICANT: KIKUCHI, MAMORU
 ; APPLICANT: KOYAMA, YASUJI
 ; TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
 ; TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A
 ; TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINYLATED AND A BIOLUMINESCENT
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/460, 934
 ; FILING DATE: 05-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIORITY INFORMATION DATA:
 ; APPLICATION NUMBER: JP 193798/1994
 ; FILING DATE: 27-JUL-1994
 ; PRIORITY INFORMATION DATA:
 ; APPLICATION NUMBER: JP 54625/1995
 ; FILING DATE: 14-MAR-1995
 ; PRIORITY INFORMATION DATA:
 ; APPLICATION NUMBER: JP 98857/1995
 ; FILING DATE: 24-APR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OBLON, NORMAN F.
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 7126-001-0
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-413-3000
 ; TELEFAX: 703-413-2220
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1704 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..1704
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 1..1704
 ; OTHER INFORMATION: /note= "Nucleotide sequence of the

OTHER INFORMATION: biotinylated firefly luciferase gene contained in recombinant
; OTHER INFORMATION: plasmid pHL203 DNA*
US-08-460-934-5

Query Match 98.5%; Score 1619.6; DB 1; Length 1704;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1625; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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DB 131 CTGCTGAGACAAATGGCGCAGATATATGATGATGATGCAAAACCTGGAGCAATGGCT 190
QY 131 ttactaaagcactaccggtgtcgattatagtcacgcgaactatagaanaacatgct 190
DB 191 TTACTAAGCGACCTTACCGGTGTGATTTATACGTACGCCCAATATTAGAAAATCATGCT 250
QY 191 gtctagagagagccttaagaatltatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 250
DB 251 GCTTAGAGAGAGCCTTTAAAGAAATTTGGTTGTGTGTGTGTGTGTGTGTGTGTGTGCA 310
QY 251 gtgaacactgtgaagaatcttcttcttcttcttcttcttcttcttcttcttcttct 310
DB 311 GTGAAGACGTGAAGATTTCTTTATTCGTATAGCGGTTTATTTAAGTGTGCGGTG 370
QY 311 tggctcccaactaagatgatttaacactacgtgaatgtgtcgaagtttagacatcctca 370
DB 371 TGGCTCAACTAATGAGATTTACCTTACGTGGAATTTGGTTCAGTTTACGATCTCTCA 430
QY 371 agccaacatgtattgtcttcttaaaagaatagataaagtttaactgttacaataa 430
DB 431 AGCCACAAATGTATTTAGTTCTTAAAGAAAGATTGATTAAGTTTATACCTGACAAA 490
QY 431 cgtgaactgtctatataaaacatgtcttcttcttcttcttcttcttcttcttcttct 490
DB 491 CGGTAACTGCTATTTAAACCATTTGTTATTTGACAGCAAGTGTATATAGAGTTATC 550
QY 491 aatcattagacactttttaaataaaacacacacacacacacacacacacacacacac 550
DB 551 AATCCATGACAACTTTATTTAAAGAAACCTCCACAAAGTTTCAAGGATCAAGTTTAA 610
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DB 1631 TACCTTAAGGCTCACTGTGTAAATTTGACGTTAAAGCAATTTAGAGAAATTTGAGAAAC 1690
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DB 1691 CAGTGTCTAAGATG 1704

RESULT 7
US-08-782-118-5
; Sequence 5, Application US/08782118
; Patent No. 5843746

GENERAL INFORMATION:
APPLICANT: TATSUMI, HIROKI
APPLICANT: FUKUDA, SATOSHI
APPLICANT: KIKUCHI, MAMORU
APPLICANT: KOYAMA, YASUJI
TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINYLATED AND A BIOLUMINESCENT
TITLE OF INVENTION: ANALYSIS METHOD
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: OBLO, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P. C. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/782,118
FILING DATE: 13-JAN-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/460,934
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: JP 193798/1994
FILING DATE: 27-JUL-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 54625/1995
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 98857/1995
FILING DATE: 24-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7126-001-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1704 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1704
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..1704
OTHER INFORMATION: /note= "Nucleotide sequence of the
OTHER INFORMATION: biotinylated firefly luciferase gene contained in recombinant
OTHER INFORMATION: plasmid pHLf203 DNA"
US-08-782-118-5

Query Match 98.5%; Score 1619.6; DB 2; Length 1704;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1625; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy 131 ttaactaacgaactacgggtgtcgaattatcgaatgcgcgaactactgaanaatcatgct 190
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DB 1261 CACACCGGAGATATTGATATTATGATGAAGAAAAACATTTCTTATGTCGATCGTTG 1320
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RESULT 10
US-08-076-042-1
; Sequence 1, Application US/08076042
; Patent No. 5330906
; GENERAL INFORMATION:
; APPLICANT: KAJIYAMA, NAOKI
; APPLICANT: NAKANO, EITICHI
; TITLE OF INVENTION: MUTANT LUCIFERASE OF A FIREFLY, MUTANT
; TITLE OF INVENTION: LUCIFERASE GENES, NOVEL RECOMBINANT DNAs CONTAINING THE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: N.Y.
; COUNTRY: U.S.A
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,042
; FILING DATE: 15-JUN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/675,211
; FILING DATE: 26-MAR-1991
; NAME: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-026-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1644 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Luciola cruciata
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1644
; US-08-076-042-1

Query Match      82.6%; Score 1357.6; DB 1; Length 1644;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1465; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

OY 1 atggaanaaatgagagacatgaanaatatgtgtatgctcgtgaacatttacctatt 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 ATGGAAACAATGGAAGAAACATGAATAATTGATGAGTGCACCTAAACGTTTAACTTATC 60
OY 61 gaagaggatctgtgagacaaattgccaagtatatgatacogatatgcaaaacttga 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 GAAGAGGATCTGTGCGAACAATTAACCAATTAACATGAGCGATATGCAAAACTTGGCG 120
OY 121 gcaattgcttactaacgacacttaccggtgtcgaattacgatacgaacgaattagaa 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 GCAATTGCTTTTACAAATGCAGTACTGAGTTGATTTATCTTACGCGCAATTACTTGAG 180
OY 181 aatcatcgtctcaggaagagctttaagaatatgtgtgtgtgtgtatgtaagaatt 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 AATCATGTTGCTTAGGAAACGCTTTCGCAAAATTATGTTGTTGTTGTTGATGCGCAATT 240
OY 241 gcggtatgcagtgaanaactgtgaagaattcttattctcgtatagccggttattata 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 GCGTTATGCAAGTGAAGAACTGTGAAGAATTTTATTCGTAAATAGCCGACTGTTTATA 300
OY 301 ggtgcggtgtggtcccaactaatgagattcacctctacgtaaggaattgttacaagtt 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 301 GGTGTAGGTGTTGACCAACCACTAATGATTTACCTTTTACGTAAGTGTGTTACAGTTTA 360
OY 361 ggcactctcaagccaacaattgtattatgtcttaaaaaaggaatgataaatttaact 420
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DB 361 GGTATCTCTAAACCAACATTTATTTAGTTCTTAAAAAAGCGTTAGATTAATTTATACA 420
OY 421 gtacaaaaaacgttaactgtctataaaacattgttataatttgacagcaagttgattat 480
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DB 421 GTACAGAAAACAGTAACACTATTAACCAATTTATTAAGTATGATAGCAAAAGTATATAT 480
OY 481 agaggttataatccatgagacactttataaaaaaacaccccaaggtttcaagaaga 540
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 481 CGAGATATCAATGTTCTGACACCTTTATTAAGAAACACACACACGAGTTTCAAGCA 540
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QY 541 tcaagttttaaactgttagaagttaccgcaagaacaaagttgctctataatgaactct 600
 Db 541 TCCAGTTTCAAACGTGGAGAGTTGACCGTAAACAGCAAGTGTCTTATATCAACTCT 600
 QY 601 tctgggttcaacccggtttgccaagaagtgtaacttaactcaatgaatcgcactaga 660
 Db 601 TCGGGTCTTACCGGTTTGGCCAAAAGGCGTACAACTTACTACGAAATATACGACTAGA 660
 QY 661 tttctcaagcttagaagttcaattatggaacaaagttccacagcagcgactttta 720
 Db 661 TTTTCTATGCTTAGAGATCCGATTATGATACCAAGTTTCCACAGGCGCGCTGTTTAA 720
 QY 721 actgtagaactccatccatggttggtatgttactacttaactgaacttaactgtg 780
 Db 721 ACTGTGCTTCATTCATCATGAGTTTGGTATGTTCACTACTCTAGGGTATTTAATTTGT 780
 QY 781 ggtttcgtatgtcatgtttaaagaaatltgaacgaagagactttttaaacaactgcaa 840
 Db 781 GGTTTTGGTGTGTTAATGTTTAACAAAATGCGATGAGAAACATTTTAAAACTCTACAA 840
 QY 841 gattacaagaatgttcaagcgttatctctgtaccgactgtgttgcaattcctaagaat 900
 Db 841 GATTATAATGTACAAAGTGTATCTGTACCGACTGTGTTGCAATTTCTCAACAAAGT 900
 QY 901 gaattactcgaataatgtatlttaacaatttagtgaattgaatcgtgcgagacact 960
 Db 901 GAATTACTCAATTAATATGATGATTTGTCAAAATTTAGTTAGATTCGATCTGGCGAGCCT 960
 QY 961 ttatctaaagaanaatgtgtaagcgtgtgtagacgttlttaactccgaggtgtgtcgtcaa 1020
 Db 961 TTATCAAAAGAAAGTGTGGAAGCTGTTGCTAGACGCTTTAATCTCCGGGTGTGCTCAA 1020
 QY 1021 ggtcgtatgtttaaagaacaaactctgtcaattatatacacaacggaagcgatgataaa 1080
 Db 1021 GGTATGCTTTTAAACAGAAACACATCTGCCATTTATTTACACCAAGAGGAGAGATATAA 1080
 QY 1081 ccaggtgcttgcgcaagatgtgcatattttaaagcaaaagttatcgatctgtgact 1140
 Db 1081 CCAGGAGCTTCTGGAAGAAAGTGTGCGCTGTTTAAAGCAAAAGTTATTTGATCTTGATACC 1140
 QY 1141 aaaaaaacttggcccgcaacagacgtggaagaagttgtgtaaaaggttcctatgctatg 1200
 Db 1141 AAAAAATCTTTAGTCTTAAACAGACGAGGAGAAAGTTGTGTTAAAGGACCTATGCTTATG 1200
 QY 1201 aaaggtatgttagatataccgaagaacaaagaataatcatagatgtaagaagttgtgtg 1260
 Db 1201 AAAGGTTATGTAAATATTCAGAAAGCAAAAGAACTTATTTGACGAAGAAAGTTGGCTG 1260
 QY 1261 cacaacagagatattggtatcatgacgaagaacaaacttcttcatgtagatcgtgtg 1320
 Db 1261 CACACCGGAGATATTGATATTATGATGAGAAACAACTTTCTTATTTGTCGATCGTTTG 1320
 QY 1321 aagtccttaactcaatacaagaatatacgaatcaccctgctgaattagaatcgttctt 1380
 Db 1321 AAGTCTTTAATCAATATCAAAAGATACCAAGTACACCTGCGAATTAGATCCGTTCTT 1380
 QY 1381 ttgcaacatccaataattttttagatgcgaggtgtgtcgtgtccagatcctataagctgtg 1440
 Db 1381 TTTGCAACATCCATCTATCTTTGATGCTGTGCTGCCGCTTCCGTGATCCGTGAGCTGGC 1440
 QY 1441 gagcttcgagagactgtgtgtgttacttaagaagaagaataatcatgactgactgaagaagta 1500
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 QY 1501 atggaattacgttgcgtgaagttcaaatgcaaaacgttgcgtgtgtgtgtgtgtgtt 1560
 Db 1501 ATGGAATTATGTTGCAAGTCAAGTTTCAAAATGCAAAAGCTTACGTGGTGTGCTGTTT 1560
 QY 1561 gtgagcgaagtaactaaagcgtctcaacgtgtgtaaatgtaagcgttaagcaaatagaagata 1620
 Db 1561 GTGATGAAGTACCTAAAGGCTTCTTACGGAATAATTTGACGCGAGACAAATTAGAGAAATC 1620

QY 1621 ctgaagaacacagttgctlaagatg 1644
 Db 1621 CTTAAGAAACCACTGCTAAGATG 1644

RESULT 11
 US-08-757-046A-3
 ; Sequence 3, Application US/08757046A
 ; Patent No. 5876995
 ; GENERAL INFORMATION:
 ; APPLICANT: Bryan, Bruce
 ; TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/757,046A
 ; FILING DATE: 11-25-96
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/597,274
 ; FILING DATE: 02-06-96
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L.
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 6680-105B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-238-0999
 ; TELEFAX: 619-238-0062
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1644 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 1..1644
 ; OTHER INFORMATION: Luciola Cruciata Luciferase (Firefly)
 ; PUBLICATION INFORMATION:
 ; DOCUMENT NUMBER: PATENT NO.: 4,968,613
 ; US-08-757-046A-3

Query Match 82.6%; Score 1357.6; DB 2; Length 1644;
 Best Local Similarity 89.1%; Pred. No. 0;
 Matches 1465; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

QY 1 atggaacacatgagacagatgaanaatatgtatgcttccgtgaacatttaccatt 60
 Db 1 ATGGAACACATGGAAGAAACGATGAATATTTGTTGAGACTTAACCGTTTACCGTATC 60
 QY 61 gaagaggatctgctggaagcacaatltgcgaaglatatgatacgatagatgcaaaacttga 120
 Db 61 GAAGAGGATCTGCTGGAACACAAATTACGCAATATACATGAGCGATATGCAAAACTTGGC 120
 QY 121 gcaattgttcttaacgacttacggtgtgtcgtatatacgaagcgaataacttaga 180
 Db 121 GCAATTGCTTTTACAAATGCAATTGATGCTGTGATTTATTTCTTACGCCCAATTTGGAG 180
 QY 181 aaatcatgctcttagagagagcctttaaagaattatgattgtgtgtgtgtaagaatc 240

181 AAATCATGTTGCTAGGAAAGCTTTGCAAAATTAATGTTGTTGTTGATGCGCAAAAT 240
QY 99tcatgcaagtgaaacactgtgaagaattcttattccctgtaagtcgggttattata 300
Db 241 GCGTATATGAGTGAAGAACTGTACAGAAATTTTATTCCTGTAATACCCGAGCTTTATA 300
QY 99tgcggtgtgtgtcccaactaagatagatctacactcgaatgtgttccagttta 360
Db 301 GGTGATAGGTGTGCAACCCACTAATGAGATTACACTTACGTAACCTGTTCAACTTTA 360
QY 99gcatcttaagccaacaattgtatttagttcttaaaaaaggtatagataaagtataact 420
Db 361 GGTATCTTAAACCAACAATTTGATTATTTAAATAAAAGCGTTAGATTAAGTTAATAA 420
QY 99tcaaaaaacggttaacgtctatlaaacaactgttatatagtgaacgaagtgat 480
Db 421 GTCAGAAAACAGTACTACTTAAACCATTTTATCTAGATGCAAGTTGATTAAT 480
QY 99agagttatcaatccatgtgacactttlaaaaaaacactccaagaagtttcaaaaga 540
Db 481 CGAGATATATCAATGTCTGACACCTTTATTAATAAAGAAACCTCCACGAGTTTCAAGCA 540
QY 99tcaagttttaaactgttagaagtttaacgcaagaagaacagttgtcttataatgaactc 600
Db 541 TCCAGTTTCAAAACCTGTGGAAGTTGACCTAAAGAAACAAGTGTCTTATTAATGAACCT 600
QY 99tgggttcaacccggttgccaaaggtgtgcaacttaacgaagaataatgcctataga 660
Db 601 TCGGTTTACCGGTTTGCCAAAAGCGGTACAACTTACTACGAAATATACAGTCACTATA 660
QY 99tcttcacgctagagatccaaattatgaaacaaagtttcaacgcaagcggtctat 720
Db 661 TTTTCTCATAGTAGAGATCCGATTTATGTAACCAAGTTTCAACGCGCAGCGCTGTTTA 720
QY 99tctgtagtaccatccatcaatggtttgtgtatgttactacttgggtactaactgtc 780
Db 721 ACTGTCGTTCCATTCATCATGATGTTTGTATGTTACACTCTAGGGATTTTAATTTGT 780
QY 99tttctgattgtcatgtttaaagaatttgcaagaagagactttttaaacaactgcga 840
Db 781 GGTTCCTGTTGTTATGTTTAAACAAATTCGATGAAGAAACATTTTAAACCTCTACA 840
QY 99tattcaaaagtccaagcgttattctgttacccgacttggttgcgaatttctaagaagt 900
Db 841 GATTATTAATGATGACAAAGTGTATCTTGTACCGACTGTTTGCATTCATCAACAAAT 900
QY 99tgaattaccgataataatgattatcaaatattagttgaattgcatctggtggagcact 960
Db 901 GAATTACTCAATTAATATGATTTGTCAAATTTAGATTGCAATCTGCGAGACCT 960
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QY 99tclatggttttaacagaacaactctgcgaattatcaacacggaagcgatgataa 1080
Db 1021 GGTATGTGTTTAACAGAAACATCTGCAATTTATTATACCAAGAGGAGACATTA 1080
QY 99tcaagtgcttctgtgcaaaagtgtgcattatttaagcaaaaagttacgtctgatalact 1140
Db 1081 CCAGAGAGCTTTCGAAAGTGGTGCCGTTGTTAAAGCAAAAGTATTCATCTTATAC 1140
QY 99tcaaaactttgggcccgaacgaagctgtgagaagtttgttaaggtgtccctgtctt 1200
Db 1141 AAAAAATCTTTAAGTCTTAACAGACGTGAGAGTTTGTAAAGGACCTATAGCTTATG 1200
QY 99aaggttatgtagataccgaagcaacgaagagaaatcatagatgaagaagttgtgtg 1260
Db 1201 AAAGGTATGTAAATATCCAGAACCAAAAGAACTTATGAGAGAGAGAGTGGCG 1260
QY 99tcaacaggaagatatgtggtatttaagatgaagaacatttcttatcgtgacgtttg 1320

Db 1261 CACACCGAGATATTCGATATTATGATGCAAGAAAAACATTTCTTATATGTCGATCGTTG 1320
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QY 99tcaacatccaaatatttttgaatgcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1440
Db 1381 TTGCAACATCATCATATCTTTGATGCTGTGTGTCGCGGCTTCCTATCTGAGCTGGC 1440
QY 99tcttcggtggt 1500
Db 1441 GAGCTTCCAGGAGCCCTTGTGTACTGCAAAACGCAAAATATGACCAAAAGAAAGTA 1500
QY 99tggatcagttgtcgaagtttcaaatgcgaacagtttcggtgtgtgtgtgtgtgtgt 1560
Db 1501 ATGATATATGTTGCAAGTCAAGTTTCAATGCAAAACGTTTACGTGTGTGTGTGT 1560
QY 99tgaagaaagtaactaaaggtctcactgtgtaaatgacgttaagcaatagagaata 1620
Db 1561 GTGATGAAGTACCTTAAGGCTTACTGGAATAATGACGCGACAGCAATTAAGAAATC 1620
QY 99tgaagaacacagttgtctaagatg 1644
Db 1621 CTTAAGAAACAGTTGCTAAGATG 1644

RESULT 12
us-09-447-208-3
; Sequence 3, Application US/09447208
; Patent No. 6113886
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Heller Ehrman White & Mcauliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/447, 208
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 0909/135, 988
; FILING DATE: 08-17-98
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/757, 046
; FILING DATE: 11-25-96
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/597, 274
; FILING DATE: 02-06-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-450-8499
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1644 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1644
OTHER INFORMATION: Luciola Cruciata Luciferase (Firefly)
PUBLICATION INFORMATION:
US-09-447-208-3

Query Match 82.6%; Score 1357.6; DB 3; Length 1644;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1465; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

QY 1 atggagaacatggagacgatgaaatattgtatgagtcgcgaaccatttccctatt 60
Db 1 ATGGAAAACATGMAAACGATGAAATATGTGTGAGCTTAACCCGTTTACCCCTATC 60
QY 61 gaagaggatctgtgagacaaatgagcaatgataatgataatgataatgataat 120
Db 61 GAAGAGGATCTGCTGAGAACACATTTAGCAAAATACATGAGCGATATGCAAAACTTGGC 120
QY 121 gcaattgcttactaacgacactaccggtgctgattatagctgacgacatactaga 180
Db 121 GCATTTGCTTTTCAAAATGACGATTACGTTGATTTATCTTACGCCGAATCTTGAG 180
QY 181 aaatcatgctgctgaggaagagcttaagaattatggttggttgctgaggaagt 240
Db 181 AAATCATGCTGCTGAGCAAAAGCTTTCGAAAATATGTTGTTGTTGATGACGCAAT 240
QY 241 ggcattgacggtgaagaacttgaagaattcttattcttcttatttaccggttattata 300
Db 241 GCGTTATGAGTGAGTAAACCTGAGAAATTTTATCTGTAATAGCGCGAGTGTATATA 300
QY 301 ggtgctgctgctgagcaaatgataatgataatgataatgataatgataatgata 360
Db 301 GGTGTAGTGTGTCACCCACATTAATGAGATTATACCTTACGTGACGTTTCAAGTTTA 360
QY 361 ggcctctcgaagcaaaatgattatgatttcttcaaaaagagatagataatgata 420
Db 361 GGTATCTCTAAACCAACAAATTTGATTTAGTTCTTAAAGAGCTTATGATTAATACA 420
QY 421 gtacaaaacggtgaactgctatttataaaacattgattatgataatgataatgata 480
Db 421 GTACAAAACAGTAACTACTATTAAACATTTGTTATCTAGTACCAAAAGTTGATTAT 480
QY 481 agaggtatcaatcagacaaacttattataaaacacactccacaaagttccaagga 540
Db 481 CGAGGATATCAATGTGTGACACCTTTATAAAGAAACACTCCACGAGTTTCAAGCA 540
QY 541 tcaagttttaaactgtagaagttaacgcgaagaagaagttgctcttataatgacct 600
Db 541 TCAGTTTCAAAACGTGTGAAAGTTGACCGTAAGAACAAAGTTGCTTATATATGAACTCT 600
QY 601 tcgggttcaacccggttggcacaagaagtgatgaactactatcaatcaatcaatga 660
Db 601 TCGGGTTCTACCGGTTTGGCAAAAGGGGTACAACTTACTACGAAATATACAGTCTAGA 660
QY 661 ttcttcaagctagaatccaatattatgagaacaaagttccacgaagcagcgtattta 720
Db 661 TTTTCTCATGTAGATAGATCGATTATATGTAACCAAGTTTACACGACGCGGTTTATA 720
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Db 721 ACTGTGCTTCATTCATCAAGGTTTGGATGATTTCACTACTCTAGGATTTTAAATTTGT 780
QY 781 ggttctgattgacgatttaagaagaatttgaagaagaagctttttaaagaacactcaa 840
Db 781 GGTTCGTGCTGTTGATATGTTTACAAAAATTCGATGAGAAACATTTTAAAGACTCTACAA 840
QY 841 gattacaatgttcaagcgtattctgttacgacattgttgcgaattcttaagaagt 900

Db 841 GATTATTAATGTACAAGGTATCTTGTACGACCTGTTGCAATTCACAAAAGT 900
QY 901 gaattactcgaataaataatgattatcaaatattagttgaattgacatcgaggagcact 960
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QY 961 ttatcgaagaatgtgtaagcgtgttgcataagctttaaatttcaacggtgttcgtaa 1020
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Db 1141 AAAAAATCTTTAGTCTTACAGACGTGAGAGTTTGTGTAAAGACGATGCTTATG 1200
QY 1201 aaagttatgataatccagaagcaagaagaatcatagatgaagaagttggttg 1260
Db 1201 AAAGTTATGTAAATATATCAGACAGCAAAAGAACTTATGACGAAGAAAGTTGCGTG 1260
QY 1261 caacagaagataatgggtatlaagatgaagaagaacatttcttactggtgactgt 1320
Db 1261 CACACCGAGATATTTGATATATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 aagcttctaatcaatacaagaagataatcaagtaacccgctggaattgaatctgt 1380
Db 1321 AAGCTTTTATCAATATCAAAAGATATCAAGTATCAACCTGCGGAATTTAGATCCGTTCT 1380
QY 1381 ttgcaacatccaaatatttctgacggtgctgctgctgctgctgctgctgctgctg 1440
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Db 1441 GAGCTTCCAGGACCGT 1500
QY 1501 atgattacgtgtgctgataagtttcaaatgcaaaacgcttgcgtgtgtgtgtgt 1560
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QY 1561 gtgacgaagctaacaaagctcactgtaaatgaaatgacggtgaagaagaaata 1620
Db 1561 GTGATGAAAGTACCTTAAAGTCTTACTGCAAAATTTGACGCGACAGCAATTTAGAGAAATC 1620
QY 1621 ctgaagaacccggtgtgtaagt 1644
Db 1621 CTTAAAGAAACCAAGTTGCTTAAGATG 1644

RESULT 13
US-09-135-988-3
Sequence 3, Application US/09135988
Patent No. 6152358
GENERAL INFORMATION:
APPLICANT: Bryan, Bruce
TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McCauliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,988
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/757,046
FILING DATE: 11-25-96
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/597,274
FILING DATE: 02-06-96
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24727-105C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-450-8499
TELEX:
INFORMATION FOR SEQ. ID NO.: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1644 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1644
OTHER INFORMATION: Luciola Cruciata Luciferase (Firefly)
PUBLICATION INFORMATION:
US-09-135-988-3

Query Match 82.6%; Score 1357.6; DB 3; Length 1644;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1465; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

QY 1 atggaacacatgaggaagaaatattgtgtatgtctcgaacattaccctatt 60
DB 1 ATGGAAACATGGAAGAAACGATGAAATATGTAGTTGACCTTAACCGTTTACCCCTATC 60
QY 61 gaagaggagatcgtctggagacaaatctgcgaagatataatgatcgatcgatgcaaaacttga 120
DB 61 GAAGAGGAGATCGCTGGAGAACCAATTACGCAATATCATGAGCGATATGCAAAACTTGGC 120
QY 121 gcaatgcttacttaacgcgaactacgcggtgtcgatatacgtacgcgaactatagaa 180
DB 121 GCAATTCCTTTACAAATGACAGTTACTGCTGTGATTAATCTTTACGCCGAATACTTGGAG 180
QY 181 aaatcatcgtcttgagagagagccttaagaatatgtgttggctgttgatgaagaatt 240
DB 181 AAATCATCTTGTCTTGAAGAAAGCTTGGCAAAATVATGGTTGGTTGATGGCAGAAAT 240
QY 241 ggcattatcagtgaaacatgtgaagaattccttattcctgtatagccggttattata 300
DB 241 GCGTATTCAGTGAAGAACTGTGAAGAAATTTTATTCTCTGTATATGCGGACTGTTTATA 300
QY 301 ggtgtcgtgtgtgtccaaactaatgagatlltaactactacgtgaatgtgttccagttta 360
DB 301 GGTGTAGGTGTGTCACCCACTAATGAGATTTACACTTACGTAACCTGGTTCACAGTTTA 360
QY 361 ggcctcttaagccaacatgtatttagttcttaaaaaagagatgataaagttataact 420
DB 361 GGTATCTCTTAAACCAACATTTGTATTGTCTTAAAAAGCGCTTGAATAAACTTTTAAACA 420
QY 421 gtacaaaaacgtaactgctataaaccattgttataatggaacgaagtgattat 480
DB 421 GTACAGAAAACAGTACTACTATTATAAACCAATGTTATTACTAGATAGCAAAAGTTGATTAT 480

QY 481 aagagttatcaatccatgacacatttataaaaaaacatccacaaaggttccaagga 540
DB 481 CGAGATATCAATGTCGTGACACCTTATATAAAGAAACATCCACAGGATTTTCAAGCA 540
QY 541 tcaagttttaaactgttagaagttaacgcgaagaagaaggtgtcttataatgaact 600
DB 541 TCCAGTTTCAAAACGTGTGAAGTTGACCGTTAAAGAACAAAGTGTCTTTATATGAACCTGT 600
QY 601 tcgggttcaacgggttgcgaagaaggtgtgcacattaccatgaaataatcgtactaga 660
DB 601 TCGGGTTTACCGGTTTGCCAAAAGCGGTACAACTTACTACAGAAATATCAGTCACTAGA 660
QY 661 ttcttcacgctagagatccaaattatagaaacaaagttccacggcagcggtattta 720
DB 661 TTTTCTCATGCTAGAGATCCGATTTATGATTAACCAAGTTTACACGAGCCCGCTGTTTAA 720
QY 721 actgtatgacaaatccatcaatggttltgtatgttactactttaggtcatcactgt 780
DB 721 ACTGTCGTCCATTCATCATGATGTTTGTATGTTCCACTACTCTAGGGTATTTAATTTGT 780
QY 781 ggttttcgattgtcatgttlaacgaatttgacgaagaagactttttaaacaactgcaa 840
DB 781 GGTTCGTGTTGTATGTTTAAACAAATTCGATGAAGAAACATTTTAAAACTCTACAA 840
QY 841 gattacaatgttcaagcgttattctgtacgcgaactgtgttgcatttcaatlaagaagt 900
DB 841 GATTTAAATGTACAAAGTGTATTTCTGTACCGACCTGTGTTGCAATTCACAAACAAAGT 900
QY 901 gaattactcgaataaataatgattatcaaatltgaattgaattgcattcgtggagacact 960
DB 901 GAATTACTCAATTAATATACATTTGTCAAAATTTGATGAGATGTCATCTGCGCAGACACT 960
QY 961 ttatctaaagaatgtgtgaagcgtgtgtgtagaacctttaaattacccgggtgtcgtcaa 1020
DB 961 TTATCAAAAAGAGTTGTGTGAACCTGTGCTTAACACCTTTAATCTTCGCCGTTTGTCTCA 1020
QY 1021 ggcctatgttlaacagaacaaacctgtgcaattatlatcacacgggaagcgatataaa 1080
DB 1021 GGTATGTGTTTAAACGAAGAACACATCTGCCATTATATTAATTCACGAAGAGACGATAA 1080
QY 1081 ccaagtgctcttcggcgaaggtgtgtccattatllaagaagaaggtatcgttataact 1140
DB 1081 CCAGAGGCTTCGGAAGAACTCGTCGTTGTTAAAGCAAAAGTTATGATTTGATATAC 1140
QY 1141 aaaaacacttggcccgacagacgagctgtgagaagtttgytlaaaggttccatgtctatg 1200
DB 1141 AAAAAATCTTTAGTTCCTACAGACGCTGAGAAAGTTTGTGTTAAAGAGACTTATGCTTATG 1200
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DB 1201 AAAGTTATGTAAATTAATCCAGAACCAACAAAGAACTTATGACGAGAAAGGTGGCTG 1260
QY 1261 cacaagaagatattggtatgataatgaagaagaacatttcttatacgttgatcgtgtg 1320
DB 1261 CACACCGGAGATATTGAGATATTATGATGAAGAAACATTTCTTTATGTGTCATGCTGTTG 1320
QY 1321 aagctttaaataaataacaaagatatacaagtaacacatcgtcgaatttgaatcgttct 1380
DB 1321 AAGTCTTTAATTAATTAACAAAGATATCCAGATACCACTCGCGAATTTGAATCCGTTCTT 1380
QY 1381 ttgcaacatccaaatatttttgaatgcggcggtgtgcgttccatccatlaagctggt 1440
DB 1381 TTGCAACATCCATCTATCTTTGATGCTGTTGTCGGGCTTCGATCCCTTACTCTGCG 1440
QY 1441 gagcttccggagagcgtgtgtgttacttaagaagaagaatcctatgcagaagaagaagta 1500
DB 1441 GAGCTTCCAGAGAGCCGTTGTTTACTCGAAGACGGAAGAAATATATACGAAAGAAAGTA 1500
QY 1501 atggaatcgttgcagttcaagtttcaaatgcgaacagtttgcgtgtgtgttccgtttt 1560
DB 1501 ATGGAATTAATGTTGCAAGTCAAGTTCACAAATGCAAAACGTTTACGTCGTGTCGTTT 1560
QY 1561 gtgagcgaaglaactaaaggttctacgtttaaatttgacggtlaaagcaattagagaata 1620

Db 1561 GTGATGATAGTACTAAGCTTACTGCAAAAATTGACGCGCAGACCAATTAGAGAAATC 1620
Qy 1621 ctgaagaacacgttgcttaagatg 1644
Db 1621 CTTAGAAACCAAGTTGCTAGATG 1644

RESULT 14
US-09-277-716-3

; Sequence 3, Application US/09277716A
; Patent No. 6232107
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
; CURRENT APPLICATION NUMBER: US/09/277,716A
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/102,939
; EARLIER FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/089,367
; EARLIER FILING DATE: 1998-06-15
; EARLIER APPLICATION NUMBER: 60/079,624
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1644
; TYPE: DNA
; ORGANISM: Luciola cruciata
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1644)
; OTHER INFORMATION: Luciola cruciata (firefly) Luciferase
; PUBLICATION INFORMATION:
; PATENT DOCUMENT NUMBER: 4,968,613
; PATENT FILING DATE: 1988-07-26
; PUBLICATION DATE: 1990-11-06
US-09-277-716-3

Query Match 82.6%; Score 1357.6; DB 4; Length 1644;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1465; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

Qy 1 atggaacacatgaggaacgatgaataatattgtgtatgtgcttgaacatttaccctat 60
Db 1 atggaacacatgaggaacgatgaataatattgtgtatgtgcttgaacatttaccctatc 60
Qy 61 gaagaagatctgtctgagacacattgacgaatattgatatgatatgcaaaacttggaa 120
Db 61 gaagaagatctgtctgagacacattgacgaatattgatatgatatgcaaaacttgggc 120
Qy 121 gcaattccttactaacgcactaccggtgctgattacgtatgcgcgcgataacttgaag 180
Db 121 gcaattccttactaacatgacgtactcgtgtgtgtatattcttcaagccgataacttggag 180
Qy 181 aaatcatgctgtctagagagagctttaaagaatattgattgtgtgtgtgtgtgtgaagaat 240
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Qy 241 gcggtatgcagtgaaactgtgaagaattcttattccctgtatataagccggttattata 300
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Qy 301 ggttcggtgtgtgtccaaactaagattatcaccttcaagtgatgtgttccacagtta 360
Db 301 ggttcggtgtgtgtccaaactaagattatcaccttcaagtgatgtgttccacagtta 360
Qy 361 ggcattcttaagccaacattgttatattgattcttaaaaaagattatagaataagtataact 420
Db 361 ggcattcttaagccaacattgttatattgattcttaaaaaagattatagaataagtataact 420

Db 361 ggtattcttaaacccaacattgttattgattcttaaaaaaggttagataaagtataaca 420
Qy 421 gtacaaaacacgttactgtctatataaacattgttatattgagacgaagaattgattat 480
Db 421 gtacaaaacacgttactgtctatataaacattgttatattgagacgaagaattgattat 480
Qy 481 agaggttaacatccatgacacatttataaaaaaacatccacgaagtttcaaaagga 540
Db 481 agaggtatccatgtgtgtgacacatttataaaaaaacacccacgaagtttcaaaagga 540
Qy 541 tcaagttttaaactgttagaagtttaacgcgaagaacgaattgtcttataatgaacct 600
Db 541 tcaagttttaaactgttagaagtttaacgcgaagaacgaattgtcttataatgaacct 600
Qy 601 tgggttcaacgcggtttgcgaagaagttgacacttaccatgaataatattgttactaga 660
Db 601 tgggttcaacgcggtttgcgaagaagttgacacttaccatgaataatattgttactaga 660
Qy 661 ttcttcacgtctagagatccaatltatggaacacgaatttccacgaagcgttattta 720
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Qy 721 actgtatgacatccatccatgattgtgtgtatgttactactttaggtatcattactgt 780
Db 721 actgtatgacatccatccatgattgtgtgtatgttactactttaggtatcattactgt 780
Qy 781 ggtttcgtattgtcatgttataacgaatttgaacgaagaacttttaaaaaactgtcaa 840
Db 781 ggtttcgtattgtcatgttataacgaatttgaacgaagaacttttaaaaaactgtcaa 840
Qy 841 gattcaaatgttcaacgcttattcttctgacgaactttgttgaacttcaatataagaagt 900
Db 841 gattcaaatgttcaacgcttattcttctgacgaactttgttgaacttcaatataagaagt 900
Qy 901 gaattactcgaataaataatattatcaaatattgaattgaattgcattcgcgcgcacct 960
Db 901 gaattactcgaataaataatattatcaaatattgaattgaattgcattcgcgcgcacct 960
Qy 961 ttactcaagaagaattgtgaagctgtgtgttagaagcttttaatttccgcggttgcgcaa 1020
Db 961 ttactcaagaagaattgtgaagctgtgtgttagaagcttttaatttccgcggttgcgcaa 1020
Qy 1021 ggtcatgtttaaacaagaacacactctgcaattatattatcacacgcgaagcgtatgataa 1080
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Qy 1081 ccaggtgtctctgycgaagttgtgcattattttaagcaaaagtatcgtattgatact 1140
Db 1081 ccaggtgtctctgycgaagttgtgcattattttaagcaaaagtatcgtattgatact 1140
Qy 1141 aaaaaaacttggccgcgaacgaagctgtgaagaattgtgttaaaggtgtcctatgtatg 1200
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Qy 1201 aaaggtatgtatgaataatccagaagaacgaagaatlatagatgaagaagttgtgtg 1260
Db 1201 aaaggtatgtatgaataatccagaagaacgaagaatlatagatgaagaagttgtgtg 1260
Qy 1261 cacacagagataatgtgtatgaatgaagaagaacacatttcttattcgtgtgacgtgtg 1320
Db 1261 cacacagagataatgtgtatgaatgaagaagaacacatttcttattcgtgtgacgtgtg 1320
Qy 1321 aagttcttaacaaatacaagaagataccaagtaaccacccgcgaattatgaatcgttctt 1380
Db 1321 aagttcttaacaaatacaagaagataccaagtaaccacccgcgaattatgaatcgttctt 1380
Qy 1381 ttgcaacatccaaatatttttgaatgcgcggtgtgtgcggttccagatccctataagttgt 1440
Db 1381 ttgcaacatccaaatatttttgaatgcgcggtgtgtgtgcggttccagatccctataagttgt 1440
Qy 1441 gaggctccggagagctgtgtgttacttaagaagaagaacatcatgaatcgtgaagaagaagta 1500
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QY 1501 atgattacgttcctagtcgaagtttcaaaacgttgcgtggtgtccgtttt 1560
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 Db 1501 atgattatgttgcgaagtttcaaaacgttgcgtggtgtccgtttt 1560
 QY 1561 gtgacgaagtaacctaaagttcactcgtgtaaaattgacgtaagcaattagaata 1620
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 Db 1561 gtgataagtaacctaaagttcactcgtgtaaaattgacgtaagcaattagaata 1620
 QY 1621 ctgaagaacacagttcctaagatg 1644
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 Db 1621 ctgaagaacacagttcctaagatg 1644

RESULT 15
 US-08-597-274A-3
 : Sequence 3, Application US/08597274A
 : Patent No. 6247995
 : GENERAL INFORMATION:
 : APPLICANT: Bryan, Bruce
 : TITLE OF INVENTION: BIOLUMINESCENT NOVELTY ITEMS
 : NUMBER OF SEQUENCES: 14
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Brown, Martin, Haller & McClain
 : STREET: 1660 Union Street
 : CITY: San Diego
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 92101-2926
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FASTSEQ Version 1.5
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/597,274A
 : FILING DATE: 02/06/96
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER:
 : FILING DATE:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Seidman, Stephanie L
 : REGISTRATION NUMBER: 33,779
 : REFERENCE/DOCKET NUMBER: 6680-105
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 619-238-0999
 : TELEFAX: 619-238-0062
 : TELEX:
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1644 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : FEATURE:
 : NAME/KEY: Coding Sequence
 : LOCATION: 1...1644
 : OTHER INFORMATION: Luciola Cruciata Luciferase (Firefly)
 : PUBLICATION INFORMATION:
 : DOCUMENT NUMBER: 4,968,613
 : US-08-597-274A-3

Query Match 82.6%; Score 1357.6; DB 4; Length 1644;
 Best Local Similarity 89.1%; Pred. No. 0;
 Matches 1465; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

QY 1 atggaanaacatggaagcaatattgtgtatggtcctgaaccatttaccctatt 60
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 Db 1 ATGGAANAACATGGAAGCAATATTGTGTATGCTGCACTTAACCGTTTACCTTATC 60

QY 61 gaagaggaatctgctgagacacattgcgcaagatataatgacatgacaaacttga 120
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 Db 61 GAAGAGGATCTGCTGAGACACATTGCGCAAGATATGACAGGATATGCAAACTTGGC 120
 QY 121 gcaattgcttactaagcaactaccggtgcgataatgacgacgaactactaga 180
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 Db 121 GCAATTGCTTACTAAGCAACTACCGGTGCGATATGACGACGAATCTTGAG 180
 QY 181 aaatctgctgctgaggaagccttaagaattatggttggttgatggaagaatt 240
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 Db 181 AAATCTGCTGCTGAGGAAGCCTTGAAGATATGTTGTTGTTGATGCGCAAAAT 240
 QY 241 gcttatgacagtaagaactgtgaagaattcttattccgtatagccggttattata 300
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 Db 241 GCTTATGACAGTGAAGAACTGTGAAGATTTTATTCCTGTAATAGCCGAGCTTTATA 300
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 Db 301 GGTGTAGGTGTGTCCACCCTAATGAGATTTACCTTACGTGAACCTGTTTCAAGTTTA 360
 QY 361 ggcattcctgaagcgaacattgattagttctaaagaagatgataagaatt 420
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 Db 361 GGTATCTTAAACCAACATTTGATTTAGTTCTTAAAGAGCTTGAATAGTTATACA 420
 QY 421 gtacaaaacgtaactgctataaaacattgtatataatggacagcaagtggatlat 480
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 Db 421 GTACAGAAACAGTAACTCTATTTAAACATTTGTTATCTAGATAGCAAACTTGATTAT 480
 QY 481 agaagttatcaatccatggaacacttataaaacacacacacacacacacacac 540
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 Db 481 CAGGATATCAATGTCTGACACCTTTATTAAGAAACACCTCCACAGCTTTTCAAGCA 540
 QY 541 tcaagttttaaactgtagaagttacccgaagaacaggtgtccttataatgaatct 600
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 Db 601 TCGGTTTCAACCGGTTTGGCAAAAGCGTACAACTTACTACGAAATTAAGTACTAGA 660
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 Db 661 TTTTCTCATGCTGAGATCCGATTAATGTTAACCAAGTTTCCACGAGCCCTGTTTAA 720
 QY 721 actgtatcaacatccatcatggttctgtatgattactacttggcgtactactgt 780
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 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 781 GGTTCGTTGTTGATGTTTAACAAAATTCGATGAAGAAACATTTTAAACTCTACAA 840
 QY 841 gattcaaatgttcaagcgttattctgtacacgacttgttgaacattcttaagaat 900
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 Db 841 GATTATTAATGTACAGTGTATTTCTTGACCGACCTTGTGCAATCTCTCAACAAAT 900
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 Db 901 GAATTACTCAATAAATAGCATTTGTCAAAATTTAGTTGAGATTGCACTGCGGACACT 960
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 QY 1021 ggtctatggtttaaagaagaacacccctgcaattatatacaccggaagcgatataa 1080
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 Db 1021 GGTATGTTGTTTAAACAGAAACATCTGCAATTAATTAATTAACCAAGAGACATATAA 1080
 QY 1081 ccaaggtgtcctggaagaattgtgcatattatgaagcaaaagttatcgattatgact 1140
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 Db 1081 CCAGAGGCTTCTGGAAGAGTGTGCGGTTGTTTAAAGCAAAAGTTATGATCTTATAC 1140
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Db 1141 AAAAAATCTTAGTCTACAGACGCGAGAGTTGTGTAAAGACCTATGCTTATG 1200
QY 1201 aaagttatctagataatccagaagcaacaagaataatcatagatgaaggttggtg 1260
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Db 1261 CACACCGAGATATTGATATTTATGATGAGAAACATTTCTTATTTGATCGATTG 1320
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Db 1321 AAGCTTTTAAATCAAAATACAAAGGATACCAAGTACCACTGCCGATTTAGAAATCGTCTT 1380
QY 1381 ttgcaacatccaaatattttgattgacgagctgtgctgtccagatccctataagctgt 1440
Db 1381 TTGCAACATCCATCTTATCTTTGATGTGGTGTGCGCGTTCCTGATCCTGTAGCTGGC 1440
QY 1441 gagcttcgagagctgtgtgtgtacttaagaagaataatctatgactgaaaaagaagta 1500
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QY 1501 atggattacgttgctagtaagttlcaaalgcacaacggttgctggtgtgtgtgtgtt 1560
Db 1501 ATGATTTATGTTCAGAGTCAAGTTTCAATGCAAAACGTTTACGTGTGTGTGTGTGT 1560
QY 1561 gtgagcgaagtaacctaaagctcactcgttaaaatlgacggtlaagcaattagagaata 1620
Db 1561 GTGATGTAAGTACCTTAAAGCTTACTGGAATAATGACGCAAGCAATTAGAGAAATC 1620
QY 1621 ctgaagaagaaccagttgctaaagtg 1644
Db 1621 CTTAAGAAACCAAGTTGCTAAGATG 1644
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Search completed: September 6, 2002, 19:30:28
Job time: 15191 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 17:47:30 ; Search time 3537.97 Seconds
(without alignments)
6271.674 Million cell updates/sec

Title: US-09-581-241-5
Perfect score: 1644
Sequence: 1 atggaacacatgagaaacga.....agaacacagctgctaagatg 1644

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: em_estbda.*
2: em_esthum.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hlc.*
9: gb_est1.*
10: gb_est2.*
11: gb_hlc.*
12: gb_gss.*
13: em_gss_hum.*
14: em_gss_inv.*
15: em_gss_pln.*
16: em_gss_vrt.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	208.6	12.7	664	10 C83857	C83857 C83857 Dict
2	199.4	12.1	768	10 BM412281	BM412281 EST586608
3	198.2	12.1	667	9 A1486799	A1486799 EST245121
4	190.4	11.6	651	10 C90519	C90519 C90519 Dict
5	189.8	11.5	582	9 AW621420	AW621420 EST312218
6	185.8	11.3	625	9 A1485586	A1485586 EST243907
7	183.2	11.1	569	9 AW218471	AW218471 EST303654
8	181.6	11.0	522	9 A1488821	A1488821 EST247160
9	173.8	10.6	543	10 BE555239	BE555239 EST7410.Y
10	173.6	10.6	612	10 BG130282	BG130282 EST475938
11	171.8	10.5	606	10 BI923203	BI923203 EST543107
12	165.6	10.1	741	9 AU214129	AU214129 AU214129
13	162.4	9.9	535	9 AL389862	AL389862 MCB57H09
14	162.2	9.9	498	10 B1425803	B1425803 sah72f03.
15	162.2	9.9	570	10 BG791252	BG791252 ESTFN115
16	161.4	9.8	548	10 BM188336	BM188336 sa399f03.
17	159.4	9.7	604	9 AU219684	AU219684 AU219684

18	159.4	9.7	604	9 AV558307	AV558307 AV558307
19	158.8	9.7	520	10 B1269977	B1269977 NF003D02F
20	158.8	9.7	638	9 AU214473	AU214473 AU214473
21	158.2	9.6	712	9 AW349844	AW349844 GM210006A
22	158	9.6	611	10 B1129072	B1129072 B1129072
23	157.8	9.6	644	10 B1309413	B1309413 EST530823
24	157.8	9.6	722	10 B139943	B139943 B139943
25	157.6	9.6	590	9 AW329421	AW329421 N2006566
26	157.4	9.6	558	9 AV680327	AV680327 AV680327
27	157.4	9.6	567	10 BG580544	BG580544 EST482271
28	157.4	9.6	656	9 AW691106	AW691106 NF041C08S
29	154.8	9.4	410	10 BM109695	BM109695 EST557231
30	154.8	9.4	977	12 CNS01MDU	AL150803 Anopheles
31	152.2	9.3	808	9 AW348381	AW348381 GM210002A
32	150.2	9.1	540	9 A1771202	A1771202 EST525298
33	149.6	9.1	506	9 AW332800	AW332800 se10d11.Y
34	149.2	9.1	529	10 BM143081	BM143081 sa139c03.
35	148.8	9.1	377	9 A1938631	A1938631 sb56d11.Y
36	148.8	9.1	655	9 AW560940	AW560940 EST315888
37	148.6	9.0	453	10 BF005122	BF005122 EST433620
38	148.6	9.0	495	9 A1284477	A1284477 4A3B-AAx-
39	147	8.9	683	10 BF492687	BF492687 AT01136.3
40	146.2	8.9	565	10 BF330067	BF330067 s073a05.Y
41	145.8	8.9	665	10 BF200141	BF200141 WHE2252_E
42	145.8	8.9	595	9 AW329094	AW329094 N200300e
43	144.6	8.8	623	10 BF634495	BF634495 NF062B09D
44	144.6	8.8	501	10 BG882703	BG882703 sae51e04.
45	144.4	8.8			

ALIGNMENTS

RESULT 1
C83857 664 bp mRNA linear EST 28-APR-1999
LOCUS C83857 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
DEFINITION C83857 Dictyostelium cDNA clone SSA391, mRNA sequence.
ACCESSION C83857
KEYWORDS C83857.1 GI:2706789
SOURCE EST.
ORGANISM Dictyostelium discoideum.
REFERENCE Dictyostelium discoideum.
AUTHORS Dictyostelium discoideum
1 (bases 1 to 664)
Morioto, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M.,
Yoshino, R., Mittra, B.N., Pl.M., Saito, T., Takemoto, K., Yasukawa, H.,
Williams, J., Maeda, M., Takeuchi, T., Ochiai, H. and Tanaka, Y.
The Dictyostelium developmental cDNA project: generation and
analysis of expressed sequence tags from the first-finger stage of
development
JOURNAL DNA Res. 5 (6), 335-340 (1998)
MEDLINE 99156227
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402nuesakura.cc.tsukuba.ac.jp
PROJECT - 'Dictyostelium discoideum cDNA project in Japan'
POLYA-No. Location/Qualifiers

FEATURES
source
1..664
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SSA391"
/clone_id="Dictyostelium discoideum SS (H.Urushihara)"
/dev_stage="slug"
BASE COUNT 234 a 105 c 124 g 201 t
ORIGIN

Query Match 12.7%; Score 208.6; DB 10; Length 664;

Db 752 GAAGTGAAGGATTCAT 768

RESULT 3

LOCUS A1486799

DEFINITION EST245121 tomato ovary, TAMU Lycopersicon esculentum cDNA clone

ACCESSION cLED11D3. mRNA sequence.

VERSION A1486799

KEYWORDS A1486799.1 GI:4382170

SOURCE EST.

ORGANISM tomato.

Lycopersicon esculentum

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Asteridae: euasterids I: Solanales: Solanaceae: Solanum;

Lycopersicon.

1 (bases 1 to 667)

Alcala, J., Vredalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upson, J., Rongning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.W., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni, J.

Generation of ESTs from tomato carpel tissue

Unpublished (1999)

CONTACT: CUGI

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>.

Location/Qualifiers

1..667

/organism="Lycopersicon esculentum"

/cultivar="T496"

/db_xref="taxon:4081"

/clone_1lb="cLED11D3"

/clone_1lb="tomato ovary, TAMU"

/tissue_type="carpel"

/dev_stage="5 days pre-anthesis to 5 days post-anthesis"

/lab_host="XLI-Blue MRF"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; CLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector Lambda Zap II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."

BASE COUNT 201 a 120 c 155 g 191 t

ORIGIN

Query Match 12.1%; Score 198.2; DB 9; Length 667;

Best Local Similarity 57.6%; Pred. No. 3.2e-35;

Matches 384; Conservative 0; Mismatches 268; Indels 15; Gaps 1;

QY 838 caagatacaaaagtcgaagcgtatctgtaccgactgtgtgcaatcctaataga 897

DB 1 CAAATTTACAGAGTGAGGCGCATTTGTGCACCTATTGTGGCTATTGCTAAG 60

QY 898 agtgaataacgcgaataatgatattatcaaatagttgaattgcatcgtggcgagca 957

DB 61 AGTCTTAGTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120

QY 958 ccttatcctaagaataatgtgtagcgtgtgtagcgtgtttaaattcaacgggtgtcgt 1017

DB 121 CCATTAGGAAAGAACTTGAAGACACGTGTGAGCACAATTTCCATAATGCTAAACTTGGT 180

QY 1018 caagcgtatgttcaacgaacaaacctcgtcaattatcatcacacgggaagcgatga- 1076

DB 181 CAAGGTTACGGATGACGAAGCCGACCAAGTGTGGCTATTGCTGCTTTGCTTAA 240

QY 1077 -----taaacccaggtgtctctgcaaaagtcgtgcatcatttaagaacaaa 1122

DB 241 GACCCCTTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 300

QY 1123 gtatcagatcttgatactaaacaaacttgggcccagacagacgttggagaattgtgta 1182

DB 301 ATTGTGATCCTTGATCTGACCAATCTCTCCAGAACCAATCTGAGAGATTGTATA 360

QY 1183 aaggtgccatgcttataagaaggttatgtagataatccgaagcacaagaagaatcata 1242

DB 361 AGAGGGATCAAAATTTATGAAGGTTACCTTAATGATCCAGAGCCACTACGGGAACAATA 420

QY 1243 gataagaaggtgtgtgacacagagagatattggattatgaagaagaacaaatttc 1302

DB 421 GACCAAGAAAGAGTGTTTACATACGGGCAATTTGGTTATATTGACATCATATGACGTT 480

QY 1303 ttatcgtgtagcgttctgaagcttctaatacaatacaagaagatalcaagctacgtct 1362

DB 481 TTGATTGTGATGCTTTAAAGAAATGATTAATAACAAAGATTCAGATGCTCCTGCT 540

QY 1363 gaattgaatcgttcttcttgcaacatccaataatlttgatgcccggcgtgctgagct 1422

DB 541 GAACCTTGAAAGCCCTTCTCCATCATCCCAATATTTCAGATGCTGCTTTTCAATG 600

QY 1423 ccagatccatagatcgtgtagcgttccggagcgtgtgttacttaagaagaagaatct 1482

DB 601 AAAGACGACGACACGACGACAGATTCTCTGTGCTTTTGTTCAGATCAATGGCTCCACA 660

QY 1483 atgactgt 1489

DB 661 ATTACTG 667

RESULT 4

LOCUS C90519

DEFINITION C90519 Dictyostellium discoideum SS (H. Urushihara) Dictyostellium

ACCESSION C90519

VERSION C90519.1 GI:3060139

KEYWORDS EST.

SOURCE Dictyostellium discoideum.

ORGANISM Dictyostellium discoideum.

REFERENCE 1 (bases 1 to 651)

Morito, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B.N., Pl, M., Saito, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.

Developmental cDNA in Dictyostellium discoideum

Unpublished (1998)

TITLE

JOURNAL

CONTACT: Hideko Urushihara

Institute of Tsukuba

University of Tsukuba

3-3-10 Ten-noda, Tsukuba, Ibaraki 305, Japan

Email: d402huesakura.cc.tsukuba.ac.jp.

Location/Qualifiers

1..651

/organism="Dictyostellium discoideum"

/strain="Ax4"

/db_xref="taxon:44689"

/clone_1lb="SSI661"

/dev_stage="slug"

BASE COUNT 251 a 83 c 110 g 207 t

ORIGIN

Query Match 11.6%; Score 190.4; DB 10; Length 651;

Best Local Similarity 62.6%; Pred. No. 2e-33;

Matches 313; Conservative 0; Mismatches 186; Indels 1; Gaps 1;

QY 1117 gcaaaagatcagatcttgatactaaacaaacttgggcccgaacagacgttggagaagt 1176

DB 1 GCTTAATTCATCTCTTACAGACCTGCTGAGAAATTAATTAATTAATTAATTAATTA 60

QY 1177 ttgttaaggttctatgcttatagaaggttatgttatgatatcaagaagaagaagata 1236

FEATURES	SOURCE
1	582
2	Location/Qualifiers
3	1. 582
4	/organism="Lycopersicon esculentum"
5	/cultivar="74496"
6	/db_xref="taxon:4081"
7	/clone="clexlin8"
8	/clone_lib="tomato root during/after fruit set, Cornell University"
9	/tissue_type="root"
10	/dev_stage="plants during and after fruit-set"
11	/note="vector: pBluescript SK(-): Site 1: EcoRI, Site 2: XhoI; supplier: Tankley; tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY 14850)."
12	181 a 99 c 146 g 156 t

Query Match	Similarity	11.5%	Score 189.8	DB 9	Length 582
Best Local	Similarity	60.6%	Pred No. 2.6e-33		
Matches 330	Conservative	0	Mismatches 212	Indels 3	Gaps 1
QY	1079	aaccagatgcttccttggcaaaagtgtgcccattttaaagaacaaagttatcgaatttgata	1138		
Db	2	AATCAAGGAGCATATGTGTACCGTTGTGAGAAACGACGAGATGAAATTTGTGATCCGATA	61		
QY	1139	ctcaaaaacacttgggcccgaacagacgctggagaagtgtgtglaaaggctctatgctta	1198		
Db	62	CGGGTTGCTCTCTGCCCTTAACCAACCCGGTGAATTTTGATTTGAGGTGATCAAAATTA	121		
QY	1199	tgaagatctatgtagataatccagaagaacacagaagaatactatagatgaagaagttggt	1258		
Db	122	TGMAAGGTACTTGATGATGACCCCTGAAGCTACAGCTAGAACATATAGAAAAAGAGATGCT	181		
QY	1259	tgcacacaggaatattggtgtatctacgatgaaagaaaacacttcttatcgttgatcgtt	1318		
Db	182	TACACTCTGGCATATTTGGATATTTGACGATGATGATGAGCTTTTCACTGGATCGAT	241		
QY	1319	tgaagctttaaataatacaagaagatatacaagtaaccacttctgaatagatcgttctc	1378		
Db	242	TGAAGGAATTTGATCAATATCAAAAGATTTCAAGTGGCGCTCTTAACCTCGAAGCACTTC	301		
QY	1379	tttggcaacatccaaataattttgattgctgcgcgcgttgcgttgcgttccatcctatagctg	1438		
Db	302	TTGTCAACACACCCCTAAACATTTCTGATGCTGCTGTGTGCCATGGAAGATGAACAGCG	361		
QY	1439	gtgagctctccggagagctgtgtgttgcacttaagaagaagaaactatgactgaagaagaag	1498		
Db	362	GGAAGTTTCCATGGCTTTTGTGTGTAGATCAAAATGAGATTCACATTTCTTGAGGTGAAG	421		
QY	1499	taatgattacgttgcctagcagtttcaatgcaaaagcgttgcgttggtggtgcgtt	1558		
Db	422	TGAAGATTTTCACTTCGCCAAGCAGGTGATATCTATAAGGAAAT---AAAGCTGATATTTT	478		
QY	1559	ttgttgacgaagttacctaagaagttcactcgtgtaaaattgacggttaagaacaattagagaa	1618		
Db	479	TCTGTGAGACGGTACCGAAATCTCATCAGGAAAAATTTCTGAGAAAAAGACTTAAGAGCTA	538		
QY	1619	tactg 1623			
Db	539	GACTG 543			
RESULT	6	A1485586	625 bp	mrna	linear
LOCUS	EST243907	tomato ovary, TMU Lycopersicon esculentum cDNA clone			
DEFINITION	EST243907	tomato ovary, TMU Lycopersicon esculentum cDNA clone			
ACCESSION	A1485586				
VERSION	A1485586.1	GI:4380957			
KEYWORDS	EST.				
SOURCE	tomato.				
ORGANISM	Lycopersicon esculentum				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.				
AUTHORS	1 (bases 1 to 625) Alcala,J., Vrebalov,J., White,R., Mattern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Romling,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D., and Giovannoni,J.				
TITLE	Generation of ESTs from tomato carpel tissue				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: CUGI Clemson University Genomics Institute 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html .				

FEATURES

FEATURES	source	location/Qualifiers
1..625		
/organism="Lycopersicon esculentum"		
/cultivar="TA96"		
/db_xref="taxon:4081"		
/clone="cLED7A3"		
/clone_1fb="tomato ovary, TAMU"		
/tissue.type="carpel"		
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"		
/lab_host="XLI-Blue MRF"		
/note="Vector: p Bluescript SK(-); Site_1: EcoRI; Site_2: XhoI; cLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector lambda ZAP II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively"		
BASE COUNT	197 a	112 c 146 g 169 t 1 others
ORIGIN		

LOCUS	522 bp	mrna	linear	EST 18-MAY-2003
DEFINITION	Al488821.1 tomato ovary, TAMU Lycopersicon esculentum cDNA clone			
VERSION	E8247160			
KEYWORDS	cLED18L20, mRNA sequence.			
SOURCE	Al488821			
ORGANISM	Al488821.1 GI:4384192 EST.			
	tomato.			
	Lycopersicon esculentum			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.			
REFERENCE	1 (bases 1 to 522)			
AUTHORS	Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Konning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J.			
TITLE	Generation of ESTs from tomato carpel tissue			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: CUGI			
	Clemson University Genomics Institute			
	Clemson University			
	100 Jordan Hall, Clemson, SC 29634, USA			
	Email: http://www.genome.clemson.edu/orders/index.html .			
FEATURES	location/Qualifiers			
SOURCE	1..522			
	/organism="Lycopersicon esculentum"			
	/cultivar="TA496"			
	/db_xref="taxon:4081"			
	/clone="cLED18L20"			
	/clone_lib="tomato ovary, TAMU"			
	/tissue_type="carpel"			
	/dev_stage="5 days pre-anthesis to 5 days post-anthesis"			
	/lab_host="X11-Blue MR"			
	/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; cLED - Tomato Carpel EST library. OligodT-primed directionally cloned cDNA in vector Lambda Zap II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."			
BASE COUNT	156 a 89 c 133 g 144 t			
ORIGIN				

[illegible]

Db 403 CAACGGGAGAAAGTCCAGTGGCTTTTGTGTATGATCAATGATGATCTACCAATTACTAG 462

Db 463 GATGAAGTGAAGGATTTTCATCTTCAACAGGT 494

RESULT	9
LOCUS	BE555239
DEFINITION	BE555239 543 bp mRNA linear EST 04-DEC-2001 sp67a10.71 Gm-c1045 glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1045-595 5' similar to TR:048868 048868 4-COMPARATE:COA LIGASE 2.1, mRNA sequence.
ACCESSION	BE555239
VERSION	BE555239.1
KEYWORDS	GI:9819726
SOURCE	EST. soybean.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 543)	Shoemaker, R., Keim, P., Vodkin, L., Expending, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Rittler, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterson, R., and Wilson, R.	Public soybean EST Project	Unpublished (1999)	Contact: Shoemaker R/Public Soybean EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, TivoliGen Corp, 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccre@resgen.com
High quality sequence stop: 416.

FEATURES	SOURCE	LOCATION/Qualifiers
1..543		
/organism="Glycine max"		
/db_xref="taxon:3847"		
/clone="GENOME SYSTEMS CLONE ID: Gm-cl045-595"		
/clone_1lb="Gm-cl045"		
/tissue_type="Hypocotyl, 9-10 day old etiolated seedlings"		
/lab_host="DH10B"		
/note="Vector: pBluescriptII SK+; site.1: EcoRI; site.2: XhoI; This cDNA library was constructed from mRNA isolated from etiolated hypocotyl tissue of 9-10 day old seedlings of the cultivar Williams 82. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dt) primer with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and XhoI. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."		
BASE COUNT	184 a	92 c 130 g 137 t
CRIGIN		

	Query Match	10.68;	Score 173.8;	DB 10;	Length 543;
	Best Local Similarity	59.08;	Pred. No. 1.3e-29;		
	Matches 317;	Conservative	0;	Mismatches 217;	Indels 3;
					Gaps 1;
QY	1093	ggcgaagtgtgcccattatcatttaagcgaagaatttcgactcttgatacttaaaaaaactttg	1152		

Db 7 GGAACCGTGTGTGAGAAACCGTGAAGATGAAATCGTGATACAGAAACGGGTGATTCCTT 66

Qy 1153 gccccgacagacgctgagaaagcttgctaaaggtcctatgctatgaaaggtatctatgta 1212

Db 67 CCAAGAAACAAATCCGAGAAATTTTCATTAAGAGGGGCAAAAGTCATGAAGAGATATCTTA 126

Qy 1213 gataatccagaagaacagagagaaatcatagatgaaaggttgctgacacagagagat 1272

Db 127 AATGACCCAGAGGCTACAGAGACACTATTAAGACAGAGAGATGTTTACACACAGAGAT 186

Qy 1273 attgggtatgacgtatgaagaaacattcttctatgctgtagctgcttgaagctttaa 1332

Db 187 ATTGGTTTCATTGATGATGATATGAACTCTTATGTTGATCGTTAAAGAAATGATGATC 246

Qy 1333 aaatacaagagatalcaatgacacacgtctgtaagaatctgctcttcttgcacaccca 1392

Db 247 AATATCAAAAGGATTCAGAGAGCTCTGCTGAGCTCGAAGCTTTGTTGCTGACCCA 306

Qy 1393 aatatttttgatccggtgctgctgctgctgctgctgctgctgctgctgctgctgctg 1452

Db 307 AACTTTTCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366

Qy 1453 gctgtgtgttacttaagaagaataatctatgactgaagaagaatgaaatgaaatgaaatgaa 1512

Db 367 GCAATTTGTTTAAGGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 426

Qy 1513 gctagtcagtttcaatgacaaacgttgcgtgctgctgctgctgctgctgctgctgctgctg 1572

Db 427 TCACACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483

Qy 1573 cctaaagctcctcactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 1629

Db 484 CCTTAACGACCTCTCGGCAAAATTTCTGCGAAGATTAATCTGCAAGACTTAACGAA 540

RESULT 10
Bg130292 612 bp mRNA linear EST 31-JAN-2001
LOCUS Bg130292 tomato shoot/meristem Lycopersicon esculentum cDNA clone
DEFINITION EST475938 5' sequence, mRNA sequence.
ACCESSION Bg130292
VERSION Bg130292.1 GI:12630480
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.

REFERENCE 1 (bases 1 to 612)
AUTHORS van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T.,
Hansen, C., Roming, C. and Tanksley, S.
TITLE Generation of ESTs from tomato shoot/meristem tissue
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
Location/Qualifiers

FEATURES
source 1. 612
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cTOF29J22"
/clone_1bp="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
/note="Vector: pluscript SK(-); Site_1: ECOR1; Site_2:
Xho1; Small expanding leaves from the growing tip were
taken from greenhouse plants (4-6wks old TA496). Tissue
was immediately frozen in liquid nitrogen."

BASE COUNT 189 a 104 c 137 g 182 t
ORIGIN

Query Match 10.6%; Score 173.6; DB 10; Length 612;
Best Local Similarity 61.8%; Pred. No. 1,4e-29;
Matches 294; Conservative 0; Mismatches 179; Indels 3; Gaps 1;

Qy 1148 ctttgccgacagacgctgagaaagcttgctaaaggtccctatgcttgaagaagt 1207

Db 9 CTCTCCCGGTAACCAACCCGGTGAATTTGATAGAGGTGATCAATCATGAAAGGTT 68

Qy 1208 atgtgataatccagaagaacaaagaagaatcatagatgaagaagttgctgacacag 1267

Db 69 ACTTGAATGACCTTCAACGCTACAGCTACAGATGAAAGAAAGAGAGGTTACACACTG 128

Qy 1268 gagatattggttattagatgagaagaacattcttctatgctgtagatcgcttgaagctc 1327

Db 129 GCGATATTGGATATATTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 188

Qy 1328 taataaatacaagaagatatacaagacacacgtgctgaatgaatgcttcttgcac 1387

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Qy 1508 acgttgctgacgaagtttcaaatgcaaacgttgcgtgctgctgctgctgctgctgctgctgctgctg 1567

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LOCUS Bg1923203
DEFINITION EST543107 tomato callus Lycopersicon esculentum cDNA clone
ACCESSION Bg1923203
VERSION Bg1923203.1 GI:16221846
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.

REFERENCE 1 (bases 1 to 606)
AUTHORS Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Tsai,
J., Utterback, T., Van Aken, S., Roming, C.M., Fraser, C.M., Martin,
G.B., Tanksley, S.D. and Giovannoni, J.
TITLE Generation of ESTs from tomato callus tissue (2001)
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
This tissue is available through the Clemson University Genomics
Institute
Seq primer: T3.
Location/Qualifiers

FEATURES
source 1. 606
/organism="Lycopersicon esculentum"
/cultivar="TA496"

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 741)	Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y. and Sugano,S.	A complementary view of the C.elegans genome	Unpublished (2001)	Contact: Yuji Kohara Genome Biology Lab. National Institute of Genetics Yata 1111, Mishima, Shizuoka 411, Japan Tel: 81-559-81-6854 Fax: 81-559-81-6855 Email: ykohara@lab.nig.ac.jp.
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Best Local Similarity	57.6%;	Pred. NO. 1e-27;	Matches 357;	Conservative 0; Mismatches 254; Indels 9; Gaps 3;
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Db 694	AATTTGAATAACATCCACAGAGATGTGAAATGACGGATTTCAATGGCTAGTCATCTT	635		
Oy 1060	acacgcgaaggcgatgatbaaccagtgctc--tggcaaagtgtgycattttaaa	1116		
Db 634	CCTGATTTAAGAATATCATCACCATATGGATGCCGTGGAAAACTTGCTCAAAATTGGTT	575		
Oy 1117	gcaaatgtatcatcttgtactaaaanaacttggccgcaacagcgttgagaagt	1176		
Db 574	ATGAAGATTGTGAGAACCGAAGAACGCAGACGCGTTAAACAAGAGGAAATT	515		
Oy 1177	tgtgtaaagggtccatgtcttatgaaaggttatgtatagataaacagaagaacagaa	1236		
Db 514	TGTGTCGTGGTCCAACAATATAGCTTGGATATCTCGGAAGACCAGAACAC--AGCC	458		
Oy 1237	atcataagataaagaagtttggttgacaacagagatatgtgtatttcgattgaagaaaa	1296		
Db 457	AGCAGCTCATCATGATGATGAGGCTTACACTGGAGCATTTGTTATTCCAATVGAGATGGA	398		
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